

FIGURE 1A

1	TGGAAGGGTT	AATTTACTCC	AAGAAAAGGC	AAGAAATCCT	TGATTTGTGG	GTCTATCACA
61	CACAAGGCTT	CTTCCCTGAT	TGGCAAAACT	ACACACCGGG	GCCAGGGGTC	AGATATCCAC
121	TGACCTTTGG	ATGGTGCTAC	AAGCTAGTGC	CAGTTGACCC	AGGGGAGGTG	GAAGAGGCCA
181	ACGGAGGAGA	AGACAACGT	TTGCTACACC	CTATGAGCCA	ACATGGAGCA	GAGGATGAAG
241	ATAGAGAAGT	ATTAAAGTGG	AAGTTTGACA	GCCTCCTAGC	ACGCAGACAC	ATGGCCCCGCG
301	AGCTACATCC	GGAGTATTAC	AAAGACTGCT	GACACAGAAG	GGACTTTCCG	CCTGGGACTT
361	TCCACTGGGG	CGTTCCGGGA	GGTGTGGTCT	GGGCGGGACT	TGGGAGTGGT	CAACCCTCAG
421	ATGCTGCATA	TAAGCAGCTG	CTTTTCGCCCT	GTACTGGGTC	TCTCTCGGTA	GACCAGATCT
481	GAGCTTGGGA	GCCCTCTGGC	TATCTAGGGA	ACCCACTGCT	TAAGCCTCAA	TAAAGCTTGC
541	CTTGAGTGCT	TTAAGTAGTG	TGTGCCCATC	TGTTGTGTGA	CTCTGGTAAC	TAGAGATCCC
601	TCAGACCCTT	TGTGGTAGTG	TGGAAAATCT	CTAGCAGTGG	CGCCCCAACA	GGGACCAGAA
661	AGTGAAAGTG	AGACCAGAGG	AGATCTCTCG	ACGCAGGACT	CGGCTTGCTG	AAGTGCACAC
721	GGCAAGAGGC	GAGAGGGGCG	GCTGGTGAGT	ACGCCAATTT	TACTTGACTA	GCGGAGGCTA
781	GAAGGAGAGA	GATGGGTGCG	AGAGCGTCAA	TATTAAGCGG	CGGAAAATTA	GATAAATGGG
841	AAAGAATTAG	GTTAAGGCCA	GGGGGAAAGA	AACATTATAT	GTTAAAACAT	CTAGTATGGG
901	CAAGCAGGGA	GCTGGAAAGA	TTTGCACCTA	ACCCTGGCCT	GTTAGAAACA	TCAGAAGGCT
961	GTAAACAAAT	AATAAAACAG	CTACAACCAG	CTCTTCAGAC	AGGAACAGAG	AGACTTAGAT
1021	CATTATTCAA	CACAGTAGCA	ACTCTCTATT	GTGTACATAA	AGGGATAGAG	GTACGAGACA
1081	CCAAGGAAGC	CTTAGACAAG	ATAGAGGAAG	AACAAAACAA	ATGTCAGCAA	AAAGCACAAC
1141	AGGCAAAAGC	AGCTGACGAA	AAGGTCAGTC	AAAATTATCC	TATAGTACAG	AATGCCCAAG
1201	GGCAAATGGT	ACACCAAGCT	ATATCACCTA	GAACATTGAA	TGCATGGATA	AAAGTAATAG
1261	AGGAAAAGGC	TTTCAATCCA	GAGGAAATAC	CCATGTTTAC	AGCATTATCA	GAAGGAGCCA
1321	CCCCACAAGA	TTTAAACACA	ATGTTAAATA	CAGTGGGGGG	ACATCAAGCA	GCCATGCAAA
1381	TGTTAAAGA	TACCATCAAT	GAGGAGGCTG	CAGAATGGGA	TAGGACACAT	CCAGTACATG
1441	CAGGGCCTGT	TGCAACAGGC	CAGATGAGAG	AACCAAGGGG	AAGTGACATA	GCAGGAACTA
1501	CTAGTACCCT	TCAGGAACAA	ATAGCATGGA	TGACAAGTAA	TCCACCTATT	CCAGTAGAAG
1561	ACATCTATAA	AAGATGGATA	ATTCTGGGGT	TAAATAAAAT	AGTAAGAATG	TATAGCCCTG
1621	TTAGCATTTT	GGACATAAAA	CAAGGGCCAA	AAGAACCCTT	TAGAGACTAT	GTAGACCGGT
1681	TCTTTAAAC	CTTAAGAGCT	GAACAAGCTA	CACAAGATGT	AAAGAATTGG	ATGACAGACA
1741	CCTTGTGGT	CCAAAATGCG	AACCCAGATT	GTAAGACCAT	TTTAAGAGCA	TTAGGACCAG
1801	GGGCCTCATT	AGAAGAAATG	ATGACAGCAT	GTCAGGGAGT	GGGAGGACCT	AGCCATAAAG
1861	CAAGAGTGTT	GGCTGAGGCA	ATGAGCCAAG	CAAACAGTAA	CATACTAGTG	CAGAGAAGCA
1921	ATTTTAAAGG	CTCTAACAGA	ATTATTAAAT	GTTTCAACTG	TGGCAAAGTA	GGGCACATAG
1981	CCAGAAATTG	CAGGGCCCCCT	AGGAAAAAGG	GCTGTTGGAA	ATGTGGACAG	GAAGGACACC
2041	AAATGAAAGA	CTGTACTGAG	AGGCAGGCTA	ATTTTTTAGG	GAAAATTG	CCTTCCCACA
2101	AGGGGAGGCC	AGGGAATTTT	CTCCAGAACA	GACCAGAGCC	AACAGCCCCA	CCAGCAGAAC
2161	CAACAGCCCC	ACCAGCAGAG	AGCTTCAGGT	TCGAGGAGAC	AACCCCCGTG	CCGAGGAAGG
2221	AGAAAGAGAG	GGAACCTTTA	ACTTCCCTCA	AATCACTCTT	TGGCAGCGAC	CCCTTGCTCT
2281	AATAAAAGTA	GAGGGCCAGA	TAAAGGAGGC	TCTCTTAGAC	ACAGGAGCAG	ATGATACAGT
2341	ATTAGAAGAA	ATAGATTGTC	CAGGGAAATG	GAAACCAAAA	ATGATAGGGG	GAATTGGAGG
2401	TTTTATCAAA	GTAAGACAGT	ATGATCAAAT	ACTTATAGAA	ATTTGTGGAA	AAAAGGCTAT
2461	AGGTACAGTA	TTAGTAGGGC	CTACACCAGT	CAACATAATT	GGAAGAAATC	TGTTAACTCA
2521	GCTTGGATGC	ACACTAAATT	TTCCAATTAG	TCCTATTGAA	ACTGTACCAG	TAAAATTAAA
2581	ACCAGGAATG	GATGGCCCAA	AGGTCAAACA	ATGGCCATTG	ACAGAAGAAA	AAATAAAAGC
2641	ATTAACAGCA	ATTTGTGAGG	AAATGGAGAA	GGAAGGAAAA	ATTACAAAAA	TTGGGCCCTGA
2701	TAATCCATAT	AACACTCCAG	TATTTGCCAT	AAAAAAGAAG	GACAGTACTA	AGTGGAGAAA
2761	ATTAGTAGAT	TTCAGGGAAC	TCAATAAAAG	AACCAAGAC	TTTTGGGAAG	TTCAATTAGG
2821	AATACCACAC	CCAGCAGGAT	TAAAAAAGAA	AAAATCAGTG	ACAGTGCTAG	ATGTGGGGGA
2881	TGCATATTTT	TCAGTTCCTT	TAGATGAAAG	CTTCAGGAAA	TATACTGCAT	TCACCATACC
2941	TAGTATAAAC	AATGAAACAC	CAGGGATTAG	ATATCAATAT	AATGTGCTGC	CACAGGGATG
3001	GAAAGGATCA	CCAGCAATAT	TCCAGAGTAG	CATGACAAAA	ATCTTAGAGC	CCTTCAGAGC
3061	AAAAAATCCA	GACATAGTTA	TCTATCAATA	TATGGATGAC	TTGTATGTAG	GATCTGACTT
3121	AGAAATAGGG	CAACATAGAG	CAAAAATAGA	AGAGTTAAGG	GAACATTTAT	TGAAATGGGG

## FIGURE 1B

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3181 ATTTACAACA CCAGACAAGA AACATCAAAA AGAACCCCCA TTTCTTTGGA TGGGGTATGA
3241 ACTCCATCCT GACAAATGGA CAGTACAACC TATACTGCTG CCAGAAAAGG ATAGTTGGAC
3301 TGTCAATGAT ATACAGAAGT TAGTGGGAAA ATTAAACTGG GCAAGTCAGA TTTACCCAGG
3361 GATTAAAGTA AGGCAACTCT GTAAACTCCT CAGGGGGGCC AAAGCACTAA CAGACATAGT
3421 ACCACTAACT GAAGAAGCAG AATTAGAATT GGCAGAGAAC AGGGAAATTT TAAGAGAACC
3481 AGTACATGGA GTATATTATG ATCCATCAAA AGACTTGATA GCTGAAATAC AGAAACAGGG
3541 GCATGAACAA TGGACATATC AAATTTATCA AGAACCATT TAAAATCTGA AAACAGGGAA
3601 GTATGCAAAA ATGAGGACTA CCCACACTAA TGATGTAAAA CAGTTAACAG AGGCAGTGCA
3661 AAAAATAGCC ATGGAAAGCA TAGTAATATG GGGAAAGACT CCTAAATTTA GACTACCCAT
3721 CCAAAAAGAA ACATGGGAGA CATGGTGGAC AGACTATTGG CAAGCCACCT GGATCCCTGA
3781 GTGGGAGTTT GTTAATACCC CTCCCCTAGT AAAATTATGG TACCAACTAG AAAAAGATCC
3841 CATAGCAGGA GTAGAACTT TCTATGTAGA TGGAGCAACT AATAGGGAAG CTAAATAGG
3901 AAAAGCAGGG TATGTTACTG ACAGAGGAAG GCAGAAAATT GTTACTCTAA CTAACACAAC
3961 AAATCAGAAG ACTGAGTTAC AAGCAATTCA GCTAGCTCTG CAGGATTCAG GATCAGAAGT
4021 AAACATAGTA ACAGACTCAC AGTATGCATT AGGAATCATT CAAGCACAAC CAGATAAGAG
4081 TGA CTCAGAG ATATTTAACC AAATAATAGA ACAGTTAATA AACAAGGAAA GAATCTACCT
4141 GTCATGGGTA CCAGCACATA AAGGAATTGG GGGAAATGAA CAAGTAGATA AATTAGTAAG
4201 TAAGGGAATT AGGAAAGTGT TGTCTCTAGA TGGAATAGAT AAAGCTCAAG AAGAGCATGA
4261 AAGGTACCAC AGCAATTGGA GAGCAATGGC TAATGAGTTT AATCTGCCAC CCATAGTAGC
4321 AAAAGAAATA GTAGCTAGCT GTGATAAATG TCAGCTAAAA GGGGAAGCCA TACATGGACA
4381 AGTCGACTGT AGTCCAGGGA TATGGCAATT AGATTGTACC CATTTAGAGG GAAAAATCAT
4441 CCTGGTAGCA GTCCATGTAG CTAGTGGCTA CATGGAAGCA GAGGTTATCC CAGCAGAAAC
4501 AGGACAAGAA ACAGCATATT TTATATTAAA ATTAGCAGGA AGATGGCCAG TCAAAGTAAT
4561 ACATACAGAC AATGGCAGTA ATTTTACCAG TACTGCAGTT AAGGCAGCCT GTTGGTGGGC
4621 AGGTATCCAA CAGGAATTTG GAATCCCTA CAATCCCCAA AGTCAGGGAG TGGTAGAATC
4681 CATGAATAAA GAATTAAAGA AAATAATAGG ACAAGTAAGA GATCAAGCTG AGCACCTTAA
4741 GACAGCAGTA CAAATGGCAG TATTCATTCA CAATTTTAAA AGAAAAGGGG GAATTGGGGG
4801 GTACAGTGCA GGGGAAAGAA TAATAGACAT AATAGCAACA GACATACAAA CTAAAGAATT
4861 ACAAAAACAA ATTATAAGAA TTCAAAATTT TCGGGTTTAT TACAGAGACA GCAGAGACCC
4921 TATTTGGAAG GGACCAGCCG AACTACTCTG GAAAGGTGAA GGGGTAGTAG TAATAGAAGA
4981 TAAAGGTGAC ATAAAGGTAG TACCAAGGAG GAAAGCAAAA ATCATTAGAG ATTATGAAA
5041 ACAGATGGCA GGTGCTGATT GTGTGGCAGG TGGACAGGAT GAAGATTAGA GCATGGAATA
5101 GTTTAGTAAA GCACCATATG TATATATCAA GGAGAGCTAG TGGATGGGTC TACAGACATC
5161 ATTTTGAAAG CAGACATCCA AAAGTAAGTT CAGAAGTACA TATCCCATTA GGGGATGCTA
5221 GATTAGTAAT AAAACATAT TGGGGTTTGC AGACAGGAGA AAGAGATTGG CATTTGGGTC
5281 ATGGAGTCTC CATAGAATGG AGACTGAGAG AATACAGCAC ACAAGTAGAC CCTGACCTGG
5341 CAGACCAGCT AATTCACATG CATTATTTTG ATTGTTTTAC AGAATCTGCC ATAAGACAAG
5401 CCATATTAGG ACACATAGTT TTTCCTAGGT GTGACTATCA AGCAGGACAT AAGAAGGTAG
5461 GATCTCTGCA ATACTTGGCA CTGACAGCAT TGATAAAACC AAAAAAGAGA AAGCCACCTC
5521 TGCCTAGTGT TAGAAAATTA GTAGAGGATA GATGGAACGA CCCCAGAAG ACCAGGGGCC
5581 GCAGAGGGAA CCATACAATG AATGGACACT AGAGATTCTA GAAGAACTCA AGCAGGAAGC
5641 TGTCAGACAC TTTCTAGAC CATGGCTCCA TAGCTTAGGA CAATATATCT ATGAAACCTA
5701 TGGGGATACT TGGACGGGAG TTGAAGCTAT AATAAGAGTA CTGCAACAAC TACTGTTTAT
5761 TCATTTTACA ATTGGATGCC AACATAGCAG AATAGGCATC TTGCGACAGA GAAGAGCAAG
5821 AAATGGAGCC AGTAGATCCT AAATAAAGC CCTGGAACCA TCCAGGAAGC CAACCTAAAA
5881 CAGCTTGTA TAATTGCTTT TGCAAACACT GTAGCTATCA TTGTCTAGTT TGCTTTTACA
5941 CAAAAGGTTT AGGCATTTCC TATGGCAGGA AGAAGCGGAG ACAGCGACGA AGCGCTCCTC
6001 CAAGTGGTGA AGATCATCAA AATCCTCTAT CAAAGCAGTA AGTACACATA GTAGATGTAA
6061 TGGTAAGTTT AAGTTTATTT AAAGGAGTAG ATTATAGATT AGGAGTAGGA GCATTGATAG
6121 TAGCACTAAT CATAGCAATA ATAGTGTGGA CCATAGCATA TATAGAATAT AGGAAATTGG
6181 TAAGACAAAA GAAAATAGAC TGGTTAATTA AAAGAATTAG GGAAAGAGCA GAAGACAGTG
6241 GCAATGAGAG TGATGGGGAC ACAGAAGAAT TGTCAACAAT GGTGGATATG GGGCATCTTA
6301 GGCTTCTGGA TGCTAATGAT TTGTAACACG GAGGACTTGT GGGTCACAGT CTACTATGGG

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FIGURE 1c

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6361 GTACCTGTGT GGAGAGAAGC AAAAATACT CTATTCTGTG CATCAGATGC TAAAGCATAT
6421 GAGACAGAAG TGCATAATGT CTGGGCTACA CATGCTTGTG TACCCACAGA CCCCAACCCA
6481 CAAGAAATAG TTTTGGGAAA TGTAACAGAA AATTTTAATA TGTGGAAAAA TAACATGGCA
6541 GATCAGATGC ATGAGGATAT AATCAGTTTA TGGGATCAAA GCCTAAAGCC ATGTGTAAAG
6601 TTGACCCAC TCTGTGTCAC TTTAACTGT ACAGATACAA ATGTTACAGG TAATAGAACT
6661 GTTACAGGTA ATACAAATGA TACCAATATT GCAAAATGCTA CATATAAGTA TGAAGAAATG
6721 AAAAATTGCT CTTTCAATGC AACCAAGAA TTAAGAGATA AGAAACATAA AGAGTATGCA
6781 CTCTTTTATA AACTTGATAT AGTACCATT AATGAAAATA GTAACAACTT TACATATAGA
6841 TTAATAAATT GCAATACCTC AACCATACAA CAAGCCTGTC CAAAGGTCTC TTTTGACCCG
6901 ATTCTATAC ATTACTGTGC TCCAGCTGAT TATGCCGATC TAAAGTGTA TAATAAGACA
6961 TTCAATGGGA CAGGACCATG TTATAATGTC AGCACAGTAC AATGTACACA TGGAAATTAAG
7021 CCAGTGGTAT CAACTCAACT ACTGTTAAAT GGTAGTCTAG CAGAAGAAGG GATAATAATT
7081 AGATCTGAAA ATTTGACAGA GAATACCAA ACAATAATAG TACATCTTAA TGAATCTGTA
7141 GAGATTAATT GTACAAGGCC CAACAATAAT ACAAGGAAA GTGTAAGGAT AGGACCAGGA
7201 CAAGCATTCT ATGCAACAAA TGACGTAATA GGAAACATAA GACAAGCACA TTGTAACATT
7261 AGTACAGATA GATGGAATAA AACTTTACAA CAGGTAATGA AAAAATTAGG AGAGCATTTT
7321 CCTAATAAAA CAATAAAATT TGAACCAAGT GCAGGAGGGG ATCTAGAAAT TACAATGCAT
7381 AGCTTTAATT GTAGAGGAGA ATTTTCTAT TGCAATACAT CAAACCTGTT TAATAGTACA
7441 TACTACCCTA AGAATGGTAC ATACAAATAC AATGGTAATT CAAGCTTACC CATCACACTC
7501 CAATGCAAAA TAAACAAAT TGTACGCATG TGGCAAGGGG TAGGACAAGC AATGTATGCC
7561 CCTCCCATG CAGGAACAT AACATGTAGA TCAAACATCA CAGGAATACT ATTGACACGT
7621 GATGGGGGAT TTAACAACAC AAACAACGAC ACAGAGGAGA CATTACAGAC TGGAGGAGGA
7681 GATATGAGGG ATAAGTGGAG AAGTGAATTA TATAAATATA AAGTGGTAGA AATTAAGCCA
7741 TTGGGAATAG CACCCACTAA GGCAAAAAGA AGAGTGGTGC AGAGAAAAAA AAGAGCAGTG
7801 GGAATAGGAG CTGTGTTCC TGGGTTCTTG GGAGCAGCAG GAAGCACTAT GGGCGCAGCG
7861 TCAATAACGC TGACGGTACA GGCCAGACAA CTGTTGTCTG GTATAGTGCA ACAGCAAAGC
7921 AATTTGCTGA AGGCTATAGA GGCGCAACAG CATATGTTGC AACTCACAGT CTGGGGCATT
7981 AAGCAGCTCC AGGCGAGAGT CCTGGCTATA GAAAGATACC TAAAGGATCA ACAGCTCCTA
8041 GGGATTTGGG GCTGCTCTGG AAGACTCATC TGCACCACTG CTGTGCCTTG GAACTCCAGT
8101 TGGAGTAATA AATCTGAAGC AGATATTTGG GATAACATGA CTTGGATGCA GTGGGATAGA
8161 GAAATTAATA ATTACACAGA AACAATATTC AGGTTGCTTG AAGACTCGCA AAACCAGCAG
8221 GAAAAGAATG AAAAAGATT ATTAGAATTG GACAAGTGGA ATAATCTGTG GAATTGGTTT
8281 GACATATCAA ACTGGCTGTG GTATATAAAA ATATTATATA TGATAGTAGG AGGCTTGATA
8341 GGTTAAGAA TAATTTTTCG TGTGCTCTCT ATAGTGAATA GAGTTAGGCA GGGGATCTCA
8401 CCTTTGTCAT TTCAGACCCT TACCCCAAGC CCGAGGGGAC TCGACAGGCT CGGAGGAATC
8461 GAAGAAGAAG GTGGAGAGCA AGACAGAGAC AGATCCATAC GATTGGTGAG CGGATTCTTG
8521 TCGCTTGCTT GGGACGATCT GCGGAGCCTG TGCCTCTTCA GCTACCACCG CTTGAGAGAC
8581 TTCATATTAA TTGCAGTGAG GGCAGTGGAA CTTCTGGGAC ACAGCAGTCT CAGGGGACTA
8641 CAGAGGGGGT GGGAGATCCT TAAGTATCTG GGAAGTCTTG TGCAGTATTG GGGTCTAGAG
8701 CTAAAAAGA GTGCTATTAG TCCGCTTGAT ACCATAGCAA TAGCAGTAGC TGAAGGAACA
8761 GATAGGATTA TAGAATTGGT ACAAAGAATT TGTAGAGCTA TCCTCAACAT ACCTAGGAGA
8821 ATAAGACAGG GCTTTGAAGC AGCTTTGCTA TAAATGGGA GGCAAGTGGT CAAACAGCAG
8881 CATAGTTGGA TGGCCTGCAG TAAGAGAAAG AATGAGAAGA ACTGAGCCAG CAGCAGAGGG
8941 AGTAGGAGCA GCGTCTCAAG ACTTAGATAG ACATGGGGCA CTTACAAGCA GCAACACACC
9001 TGCTACTAAT GAAGCTTGTG CCTGGCTGCA AGCACAAGAG GAGGACGGAG ATGTAGGCTT
9061 TCCAGTCAGA CCTCAGGTAC CTTTAAGACC AATGACTTAT AAGAGTGCAG TAGATCTCAG
9121 CTTCTTTTTA AAAGAAAAGG GGGGACTGGA AGGGTTAATT TACTCTAGGA AAAGGCAAGA
9181 AATCCTTGAT TTGTGGGTCT ATAACACACA AGGCTTCTTC CCTGATTGGC AAAACTACAC
9241 ATCGGGGCCA GGGGTCCGAT TCCCACTGAC CTTTGGATGG TGCTTCAAGC TAGTACCAGT
9301 TGACCCAAGG GAGGTGAAAG AGGCCAATGA AGGAGAAGAC AACTGTTTGC TACACCCTAT
9361 GAGCCAACAT GGAGCAGAGG ATGAAGATAG AGAAGTATTA AAGTGGAAGT TTGACAGCCT
9421 TCTAGCACAC AGACACATGG CCCGCGAGCT ACATCCGGAG TATTACAAAG ACTGCTGACA

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FIGURE 1d

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9481 CAGAAGGGAC TTTCCGCTG GGAATTTCCA CTGGGGCGTT CCGGGAGGTG TGGTCTGGGC
9541 GGGACTTGGG AGTGGTCACC CTCAGATGCT GCATATAAGC AGCTGCTTTT CGCTTGTAAT
9601 GGGTCTCTCT CGGTAGACCA GATCTGAGCC TGGGAGCTCT CTGGCTATCT AGGGAACCCA
9661 CTGCTTAGGC CTCAATAAAG CTTGCCCTGA GTGCTCTAAG TAGTGTGTGC CCATCTGTTG
9721 TGTGACTCTG GTAAGTAGAG ATCCCTCAGA CCCTTTGTGG TAGTGTGGAA AATCTCTAGC
9781 A

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1 50

B-SF162 (1) ----MDAMKRGCLCQLLCQAVFESP-SAVEKQWVTVYYGVVPVWREAKTT  
C-TV1.8\_2 (1) GMMGTQRCQQTWVTVYYGVVPVWREAKTT  
C-TV1.8\_5 (1) GMMGTQRCQQTWVTVYYGVVPVWREAKTT  
C-TV2.12-5/1 (1) PARCILLYRHHVWVTVYYGVVPVWREAKTT  
C-MJ4 (1) LKCIPLWQQTWVTVYYGVVPVWREAKTT  
IndiaC-93IN101 (1) RRTILLYQQTWVTVYYGVVPVWREAKTT  
A-Q2317 (1) MCGIQNCCHLLTILGTIFCSAVNNWVTVYYGVVPVWREAKTT  
D-92UG001 (1) RREIEEYLCLIRVLLIGETVYVAKKWVTVYYGVVPVWREAKTT  
E-cm235 (1) ----MDAMKRGCLCQLLCQAVFESP-SASNNWVTVYYGVVPVWREAKTT  
Consensus (1) MRV G RN Q WNIWGILGFWMLM S E LWVTVYYGVVPVWREAKTT

51 100

B-SF162 (46) LCASDAKAYDEKHNVWATHACVPTDPNPCEVLGNVTEFNMWNNNDMA  
C-TV1.8\_2 (50) LCASDAKAYDEKHNVWATHACVPTDPNPCEVLGNVTEFNMWNNNDMA  
C-TV1.8\_5 (50) LCASDAKAYDEKHNVWATHACVPTDPNPCEVLGNVTEFNMWNNNDMA  
C-TV2.12-5/1 (50) LCASDAKAYDEKHNVWATHACVPTDPNPCEVLGNVTEFNMWNNNDMA  
C-MJ4 (49) LCASDAKAYDEKHNVWATHACVPTDPNPCEVLGNVTEFNMWNNNDMA  
IndiaC-93IN101 (51) LCASDAKAYDEKHNVWATHACVPTDPNPCEVLGNVTEFNMWNNNDMA  
A-Q2317 (51) LCASDAKAYDEKHNVWATHACVPTDPNPCEVLGNVTEFNMWNNNDMA  
D-92UG001 (51) LCASDAKAYDEKHNVWATHACVPTDPNPCEVLGNVTEFNMWNNNDMA  
E-cm235 (46) LCASDAKAYDEKHNVWATHACVPTDPNPCEVLGNVTEFNMWNNNDMA  
Consensus (51) LCASDAKAYETEVHNVWATHACVPTDPNPCEIVLNVTEFNMWNNNDMA

101 β2/v1v2/β3

B-SF162 (96) QMHEDIISLWDQSLKPCVKLTPLCVTLNCTHCKNATN-----TKSS  
C-TV1.8\_2 (100) QMHEDIISLWDQSLKPCVKLTPLCVTLNCTHCKNATN-----TKSS  
C-TV1.8\_5 (100) QMHEDIISLWDQSLKPCVKLTPLCVTLNCTHCKNATN-----TKSS  
C-TV2.12-5/1 (100) QMHEDIISLWDQSLKPCVKLTPLCVTLNCTHCKNATN-----TKSS  
C-MJ4 (99) QMHEDIISLWDQSLKPCVKLTPLCVTLNCTHCKNATN-----TKSS  
IndiaC-93IN101 (101) QMHEDIISLWDQSLKPCVKLTPLCVTLNCTHCKNATN-----TKSS  
A-Q2317 (101) QMHEDIISLWDQSLKPCVKLTPLCVTLNCTHCKNATN-----TKSS  
D-92UG001 (101) QMHEDIISLWDQSLKPCVKLTPLCVTLNCTHCKNATN-----TKSS  
E-cm235 (96) QMHEDIISLWDQSLKPCVKLTPLCVTLNCTHCKNATN-----TKSS  
Consensus (101) QMHEDIISLWDQSLKPCVKLTPLCVTLNCTHCKNATN-----TKSS

151 200

B-SF162 (138) NWKEMDRGTEKNCSEFKYTHSLNKMCKEYALFYLDVVEVDN-----DN  
C-TV1.8\_2 (150) GGIYNIEMKNCSEFKYTHSLNKMCKEYALFYLDVVEVDN-----DN  
C-TV1.8\_5 (150) ANATYKYEMKNCSEFKYTHSLNKMCKEYALFYLDVVEVDN-----DN  
C-TV2.12-5/1 (141) -----KMKNCSEFKYTHSLNKMCKEYALFYLDVVEVDN-----DN  
C-MJ4 (139) TSNAMKAMKNCSEFKYTHSLNKMCKEYALFYLDVVEVDN-----DN  
IndiaC-93IN101 (141) NLYNGSVEMKNCSEFKYTHSLNKMCKEYALFYLDVVEVDN-----DN  
A-Q2317 (139) -G--DRGTEKNCSEFKYTHSLNKMCKEYALFYLDVVEVDN-----DN  
D-92UG001 (144) GMENNDQIMKNCSEFKYTHSLNKMCKEYALFYLDVVEVDN-----DN  
E-cm235 (141) NIGNIETEMKNCSEFKYTHSLNKMCKEYALFYLDVVEVDN-----DN  
Consensus (151) T EEMKNCSEFKYTHSLNKMCKEYALFYLDVVEVDN-----DN

Figure 2B

	201	*		*	*	250
B-SF162	(183)	SYRLINCNTSVI	QCPK	FFPIPIHYCAPAG	VLKCDKFN	GGGC
C-TV1.8_2	(197)	TYRLINCNTSTII	QCPK	FFPIPIHYCAPAG	VLKCDKFN	GGGC
C-TV1.8_5	(197)	TYRLINCNTSTII	QCPK	FFPIPIHYCAPAG	VLKCDKFN	GGGC
C-TV2.12-5/1	(183)	NYRLINCNTSAII	QCPK	FFPIPIHYCAPAG	VLKCDKFN	GGGC
C-MJ4	(189)	EYRLINCNTSTII	QCPK	FFPIPIHYCAPAG	VLKCDKFN	GGGC
IndiaC-93IN101	(191)	EYRLINCNTSAII	QCPK	FFPIPIHYCAPAG	VLKCDKFN	GGGC
A-Q2317	(182)	EYRLINCNTSAII	QCPK	FFPIPIHYCAPAG	VLKCDKFN	GGGC
D-92UG001	(194)	NYRLINCNTSAII	QCPK	FFPIPIHYCAPAG	VLKCDKFN	GGGC
E-cm235	(188)	EYRLINCNTSVIK	QCPK	FFPIPIHYCAPAG	VLKCDKFN	GGGC
Consensus	(201)	YRLINCNTS	ITQACPKVSFDP	PIPIHYCAPAGYAILKCN	NK	FNGTGPC
	251	*		*	*	300
B-SF162	(233)	TNVSIVQCTHGI	FPVVSTQLLNGSLAEE	GIIRSNFTDN	NAKIVQLK	
C-TV1.8_2	(247)	YNVSIVQCTHGI	FPVVSTQLLNGSLAEE	GIIRSNFTDN	NAKIVQLK	
C-TV1.8_5	(247)	YNVSIVQCTHGI	FPVVSTQLLNGSLAEE	GIIRSNFTDN	NAKIVQLK	
C-TV2.12-5/1	(233)	DNVSIVQCTHGI	FPVVSTQLLNGSLAEE	GIIRSNFTDN	NAKIVQLK	
C-MJ4	(239)	NNVSIVQCTHGI	FPVVSTQLLNGSLAEE	GIIRSNFTDN	NAKIVQLK	
IndiaC-93IN101	(241)	NNVSIVQCTHGI	FPVVSTQLLNGSLAEE	GIIRSNFTDN	NAKIVQLK	
A-Q2317	(232)	KNVSIVQCTHGI	FPVVSTQLLNGSLAEE	GIIRSNFTDN	NAKIVQLK	
D-92UG001	(244)	KNVSIVQCTHGI	FPVVSTQLLNGSLAEE	GIIRSNFTDN	NAKIVQLK	
E-cm235	(238)	KNVSIVQCTHGI	FPVVSTQLLNGSLAEE	GIIRSNFTDN	NAKIVQLK	
Consensus	(251)	NVSTVQCTHGI	KFPVVSTQLLNGSLAEE	GIIRSNFTDN	NAKIVQLK	
	301	*		*	*	350
B-SF162	(283)	ESVEINCTRP	NNTKRSIRIGPGQAFYATGDIIGDIRQAH	CNIS	KWN	
C-TV1.8_2	(297)	ESVEINCTRP	NNTKRSIRIGPGQAFYATGDIIGDIRQAH	CNIS	KWN	
C-TV1.8_5	(297)	ESVEINCTRP	NNTKRSIRIGPGQAFYATGDIIGDIRQAH	CNIS	KWN	
C-TV2.12-5/1	(283)	ESVEINCTRP	NNTKRSIRIGPGQAFYATGDIIGDIRQAH	CNIS	KWN	
C-MJ4	(289)	ESVEINCTRP	NNTKRSIRIGPGQAFYATGDIIGDIRQAH	CNIS	KWN	
IndiaC-93IN101	(291)	ESVEINCTRP	NNTKRSIRIGPGQAFYATGDIIGDIRQAH	CNIS	KWN	
A-Q2317	(282)	ESVEINCTRP	NNTKRSIRIGPGQAFYATGDIIGDIRQAH	CNIS	KWN	
D-92UG001	(294)	ESVEINCTRP	NNTKRSIRIGPGQAFYATGDIIGDIRQAH	CNIS	KWN	
E-cm235	(288)	ESVEINCTRP	NNTKRSIRIGPGQAFYATGDIIGDIRQAH	CNIS	KWN	
Consensus	(301)	ESVEINCTRP	NNTKRSIRIGPGQAFYATGDIIGDIRQAH	CNIS	KWN	
	351	*		*	*	400
B-SF162	(332)	NTLQVVTKLQ	AFGNT-IVFKQSGGDPEIVMHSFNC	GGEFFYC	N	
C-TV1.8_2	(346)	NTLQVVTKLQ	AFGNT-IVFKQSGGDPEIVMHSFNC	GGEFFYC	N	
C-TV1.8_5	(346)	NTLQVVTKLQ	AFGNT-IVFKQSGGDPEIVMHSFNC	GGEFFYC	N	
C-TV2.12-5/1	(332)	NTLQVVTKLQ	AFGNT-IVFKQSGGDPEIVMHSFNC	GGEFFYC	N	
C-MJ4	(338)	NTLQVVTKLQ	AFGNT-IVFKQSGGDPEIVMHSFNC	GGEFFYC	N	
IndiaC-93IN101	(340)	NTLQVVTKLQ	AFGNT-IVFKQSGGDPEIVMHSFNC	GGEFFYC	N	
A-Q2317	(331)	NTLQVVTKLQ	AFGNT-IVFKQSGGDPEIVMHSFNC	GGEFFYC	N	
D-92UG001	(343)	NTLQVVTKLQ	AFGNT-IVFKQSGGDPEIVMHSFNC	GGEFFYC	N	
E-cm235	(337)	NTLQVVTKLQ	AFGNT-IVFKQSGGDPEIVMHSFNC	GGEFFYC	N	
Consensus	(351)	NTLQVVTKLQ	AFGNT-IVFKQSGGDPEIVMHSFNC	GGEFFYC	N	

Figure 2C

		401	*	*	*	↓	β20/β21	↓	500
B-SF162	(381)	LFNSNNNN-----TIGPN	---	TCGII	TPC	IKQI	IRWQE	GG	ANYASP
C-TV1.8_2	(395)	LFNSNNHS---N	NYKY	GNSSSPI	TCQ	IKQI	IRWQE	GG	QATYASP
C-TV1.8_5	(395)	LFNSNNYP---K	NYKY	GNSSLPI	TCQ	IKQI	IRWQE	GG	QATYASP
C-TV2.12-5/1	(382)	LFNSNN	SNGTCT	TC	CMST	---	NTERI	TCQ	IKQI
C-MJ4	(387)	LFNSNN	NS	---	TGDT	---	STII	SC	IKQI
IndiaC-93IN101	(389)	LFNSNN	MPTYMP	TESNS	---	NS	II	TC	IKQI
A-Q2317	(380)	LFNSNN	YVNSTWD	LDST	---	ES	ND	II	TC
D-92UG001	(392)	LFNSNN	AND	STW	IGNNNTGSD	NE	II	TC	IKQI
E-cm235	(386)	LFNSNN	ICIE	---	NG	IMGC	---	NG	II
Consensus	(401)	LFNSTY		NGT	N	N	TITLPCRIKQI	INMWQGVGRAMYAPP	
		451	*	*	*	*			500
B-SF162	(424)	IRGNI	IRCSSNITG	LL	LDGGKEIS	NT	---	TEIFRP	GGG
C-TV1.8_2	(442)	IAGNI	ICRSNITG	LL	LDGGFNT	NT	---	TEIFRP	GGG
C-TV1.8_5	(442)	IAGNI	ICRSNITG	LL	LDGGFNT	NT	---	TEIFRP	GGG
C-TV2.12-5/1	(430)	IAGNI	ICRSNITG	LL	LDGGDN	NT	---	TEIFRP	GGG
C-MJ4	(428)	IAGNI	ICKSNITG	LL	LDGGNET	GI	---	TEIFRP	GGG
IndiaC-93IN101	(436)	IAGNI	ICTSNITG	LL	LDGGIKEND	TENKTEIFRP	GGG		
A-Q2317	(429)	IPGV	IKCESNITG	LL	LDGGKD	NT	---	TEIFRP	GGG
D-92UG001	(441)	IEGW	INCASNITG	LL	LDGGGAND	DS	---	TEIFRP	GGG
E-cm235	(429)	IEGR	INCVSNITG	LL	LDGGAIN	NT	---	TEIFRP	GGG
Consensus	(451)	IAGNITC	SNITG	LL	LDGG	NT	N	ETFRPGGG	MDRDNWRSELY
		501							550
B-SF162	(471)	KYKVV	KIEPLG	APT	KRRVV	QREKRA	VG	IGAV	FLG
C-TV1.8_2	(489)	KYKVV	KIEPLG	APT	KRRVV	QREKRA	VG	IGAV	FLG
C-TV1.8_5	(491)	KYKVV	KIEPLG	APT	KRRVV	QREKRA	VG	IGAV	FLG
C-TV2.12-5/1	(476)	KYKVV	KIEPLG	APT	KRRVV	QREKRA	VG	IGAV	FLG
C-MJ4	(474)	KYKVV	KIEPLG	APT	KRRVV	QREKRA	VG	IGAV	FLG
IndiaC-93IN101	(486)	KYKVV	KIEPLG	APT	KRRVV	QREKRA	VG	IGAV	FLG
A-Q2317	(475)	KYKVV	KIEPLG	APT	KRRVV	QREKRA	VG	IGAV	FLG
D-92UG001	(488)	KYKVV	KIEPLG	APT	KRRVV	QREKRA	VG	IGAV	FLG
E-cm235	(475)	KYKVV	KIEPLG	APT	KRRVV	QREKRA	VG	IGAV	FLG
Consensus	(501)	KYKVV	KIEPLG	APT	KRRVV	QREKRA	VG	IGAV	FLG
		551							600
B-SF162	(521)	ITLT	QARQLLSGIVQ	QNNLL	RAIEAQQH	LL	QLT	VWGIKQLO	QARVLAVE
C-TV1.8_2	(539)	ITLT	QARQLLSGIVQ	QNNLL	RAIEAQQH	LL	QLT	VWGIKQLO	QARVLAVE
C-TV1.8_5	(541)	ITLT	QARQLLSGIVQ	QNNLL	RAIEAQQH	LL	QLT	VWGIKQLO	QARVLAVE
C-TV2.12-5/1	(526)	ITLT	QARQLLSGIVQ	QNNLL	RAIEAQQH	LL	QLT	VWGIKQLO	QARVLAVE
C-MJ4	(524)	ITLT	QARQLLSGIVQ	QNNLL	RAIEAQQH	LL	QLT	VWGIKQLO	QARVLAVE
IndiaC-93IN101	(536)	ITLT	QARQLLSGIVQ	QNNLL	RAIEAQQH	LL	QLT	VWGIKQLO	QARVLAVE
A-Q2317	(525)	ITLT	QARQLLSGIVQ	QNNLL	RAIEAQQH	LL	QLT	VWGIKQLO	QARVLAVE
D-92UG001	(538)	ITLT	QARQLLSGIVQ	QNNLL	RAIEAQQH	LL	QLT	VWGIKQLO	QARVLAVE
E-cm235	(525)	ITLT	QARQLLSGIVQ	QNNLL	RAIEAQQH	LL	QLT	VWGIKQLO	QARVLAVE
Consensus	(551)	ITLT	QARQLLSGIVQ	QNNLL	RAIEAQQH	LL	QLT	VWGIKQLO	QARVLAVE



Figure 2D

		601		*	*	*	650
B-SF162	(571)	RYLQDOGLGFWGCSG	ICTTAVWNSSWSN	LDQIWNNTWQWRE			
C-TV1.8_2	(589)	RYLQDOGLGFWGCSG	ICTTAVWNSSWSN	EKIWDNNTWQWRE			
C-TV1.8_5	(591)	RYLQDOGLGFWGCSG	ICTTAVWNSSWSN	EAIWDNNTWQWRE			
C-TV2.12-5/1	(576)	RYLQDOGLGFWGCSG	ICTTNVLWNSSWSN	QSIWDNNTWQWRE			
C-MJ4	(574)	RYLQDOGLGFWGCSG	ICTTAVWNSSWSN	QHIWDNNTWQWRE			
IndiaC-93IN101	(586)	RYLQDOGLGFWGCSG	ICTTAVWNSSWSN	QSIWNNTWQWRE			
A-Q2317	(575)	RYLQDOGLGFWGCSG	ICTTNVLWNSSWSN	LDEIWNNTWQWRE			
D-92UG001	(588)	RYLQDOGLGFWGCSG	ICTTTTAVWNSSWSN	LDDIWNNTWQWRE			
E-cm235	(575)	RYLQDOGLGFWGCSG	ICTTAVWNSSWSN	YEEIWNNTWQWRE			
Consensus	(601)	RYLKDQQLLGFWGCSG	KLICCTTAVWNSSWSNKS	DIWNNTWQWRE			
		651					700
B-SF162	(621)	ISNYTGLIINIS	SONQOEKNE	DLLELDKRWASLWNWF	IKW	WYIKI	
C-TV1.8_2	(639)	ISNYTGLIINIS	SONQOEKNE	DLLELDKRWNLWNWF	IKW	WYIKI	
C-TV1.8_5	(641)	ISNYTGLIINIS	SONQOEKNE	DLLELDKRWNLWNWF	IKW	WYIKI	
C-TV2.12-5/1	(626)	ISNYTGLIINIS	SQSQOEKNE	DLLELDKRWNLWNWF	IKW	WYIKI	
C-MJ4	(624)	ISNYTGLIINIS	SONQOEKNE	DLLELDKRWNLWNWF	IKW	WYIKI	
IndiaC-93IN101	(636)	ISNYTGLIINIS	SONQOEKNE	DLLELDKRWNLWNWF	IKW	WYIKI	
A-Q2317	(625)	ISNYTGLIINIS	SONQOEKNE	DLLELDKRWNLWNWF	IKW	WYIKI	
D-92UG001	(638)	ISNYTGLIINIS	SQSQOEKNE	DLLELDKRWNLWNWF	IKW	WYIKI	
E-cm235	(625)	ISNYTGLIINIS	SONQOEKNE	DLLELDKRWNLWNWF	IKW	WYIKI	
Consensus	(651)	ISNYTGLIINIS	SONQOEKNE	DLLELDKRWNLWNWF	IKW	WYIKI	
		701					750
B-SF162	(671)	FIMIVGGLGLRI	IFVLSINRVRQGYSP	LSQTFEARRGDRPGIE			
C-TV1.8_2	(689)	FIMIVGGLGLRI	IFVLSINRVRQGYSP	LSQTFEARRGDRPGIE			
C-TV1.8_5	(691)	FIMIVGGLGLRI	IFVLSINRVRQGYSP	LSQTFEARRGDRPGIE			
C-TV2.12-5/1	(676)	FIMIVGGLGLRI	IFVLSINRVRQGYSP	LSQTFEARRGDRPGIE			
C-MJ4	(674)	FIMIVGGLGLRI	IFVLSINRVRQGYSP	LSQTFEARRGDRPGIE			
IndiaC-93IN101	(686)	FIMIVGGLGLRI	IFVLSINRVRQGYSP	LSQTFEARRGDRPGIE			
A-Q2317	(675)	FIMIVGGLGLRI	IFVLSINRVRQGYSP	LSQTFEARRGDRPGIE			
D-92UG001	(688)	FIMIVGGLGLRI	IFVLSINRVRQGYSP	LSQTFEARRGDRPGIE			
E-cm235	(675)	FIMIVGGLGLRI	IFVLSINRVRQGYSP	LSQTFEARRGDRPGIE			
Consensus	(701)	FIMIVGGLGLRI	IFVLSINRVRQGYSP	LSQTFEARRGDRPGIE			
		751					800
B-SF162	(721)	EEGGEQDRSR	IRLVSGFLALWDDL	RLSLCLFSYHRLRDL	IFILIAAR	VEL	
C-TV1.8_2	(739)	EEGGEQDRSR	IRLVSGFLALWDDL	RLSLCLFSYHRLRDL	IFILIAAR	VEL	
C-TV1.8_5	(741)	EEGGEQDRSR	IRLVSGFLALWDDL	RLSLCLFSYHRLRDL	IFILIAAR	VEL	
C-TV2.12-5/1	(726)	EEGGEQDRSR	IRLVSGFLALWDDL	RLSLCLFSYHRLRDL	IFILIAAR	VEL	
C-MJ4	(724)	EEGGEQDRSR	IRLVSGFLALWDDL	RLSLCLFSYHRLRDL	IFILIAAR	VEL	
IndiaC-93IN101	(736)	EEGGEQDRSR	IRLVSGFLALWDDL	RLSLCLFSYHRLRDL	IFILIAAR	VEL	
A-Q2317	(725)	EEGGEQDRSR	IRLVSGFLALWDDL	RLSLCLFSYHRLRDL	IFILIAAR	VEL	
D-92UG001	(738)	EEGGEQDRSR	IRLVSGFLALWDDL	RLSLCLFSYHRLRDL	IFILIAAR	VEL	
E-cm235	(725)	EEGGEQDRSR	IRLVSGFLALWDDL	RLSLCLFSYHRLRDL	IFILIAAR	VEL	
Consensus	(751)	EEGGEQDRSR	IRLVSGFLALWDDL	RLSLCLFSYHRLRDL	IFILIAAR	VEL	

Figure 2E

	801	850
B-SF162	(771) LGH-----RGWEALKYWNLLSYWQELKNS	FFAATAVAAGTD
C-TV1.8_2	(789) LGHSTTHGQGWETIKYIGSLQYWGLELKSS	FFAATAVAAGTD
C-TV1.8_5	(791) LGHSTTHGQGWETIKYIGSLQYWGLELKSS	FFAATAVAAGTD
C-TV2.12-5/1	(776) LGHSTTHGQGWGTIKYIGSLQYWGLELKSS	FFAATAVAAGTD
C-MJ4	(774) LGHSTTHGQGWETIKYIGSLQYWGLELKSS	FFAATAVAAGTD
IndiaC-93IN101	(786) LGRSS-----RGWEALKYWNLLSYWQELKNS	FFAATAVAAGTD
A-Q2317	(775) LGHSTTHGQGWETIKYIGSLQYWGLELKSS	FFAATAVAAGTD
D-92UG001	(788) LGR-----RGWEALKYWNLLSYWQELKNS	FFAATAVAAGTD
E-cm235	(775) LGHSTTHGQGWETIKYIGSLQYWGLELKSS	FFAATAVAAGTD
Consensus	(801) LGRSSLRGL RGWEALKYLGSLQYWGLELKSS	FFAATAVAAGTD
	851	879
B-SF162	(814) RIIIEAQRIQGRFFHHIPRIRQGLERALL	
C-TV1.8_2	(839) RIIIEAQRIQGRFFHHIPRIRQGLERALL	
C-TV1.8_5	(841) RIIIEAQRIQGRFFHHIPRIRQGLERALL	
C-TV2.12-5/1	(826) RIIIEAQRIQGRFFHHIPRIRQGLERALL	
C-MJ4	(824) RIIIEAQRIQGRFFHHIPRIRQGLERALL	
IndiaC-93IN101	(829) RIIIEAQRIQGRFFHHIPRIRQGLERALL	
A-Q2317	(825) RIIIEAQRIQGRFFHHIPRIRQGLERALL	
D-92UG001	(831) RIIIEAQRIQGRFFHHIPRIRQGLERALL	
E-cm235	(825) RIIIEAQRIQGRFFHHIPRIRQGLERALL	
Consensus	(851) RIIIEAQRI RAILNIPRIRQGLERALL	



Figure 3

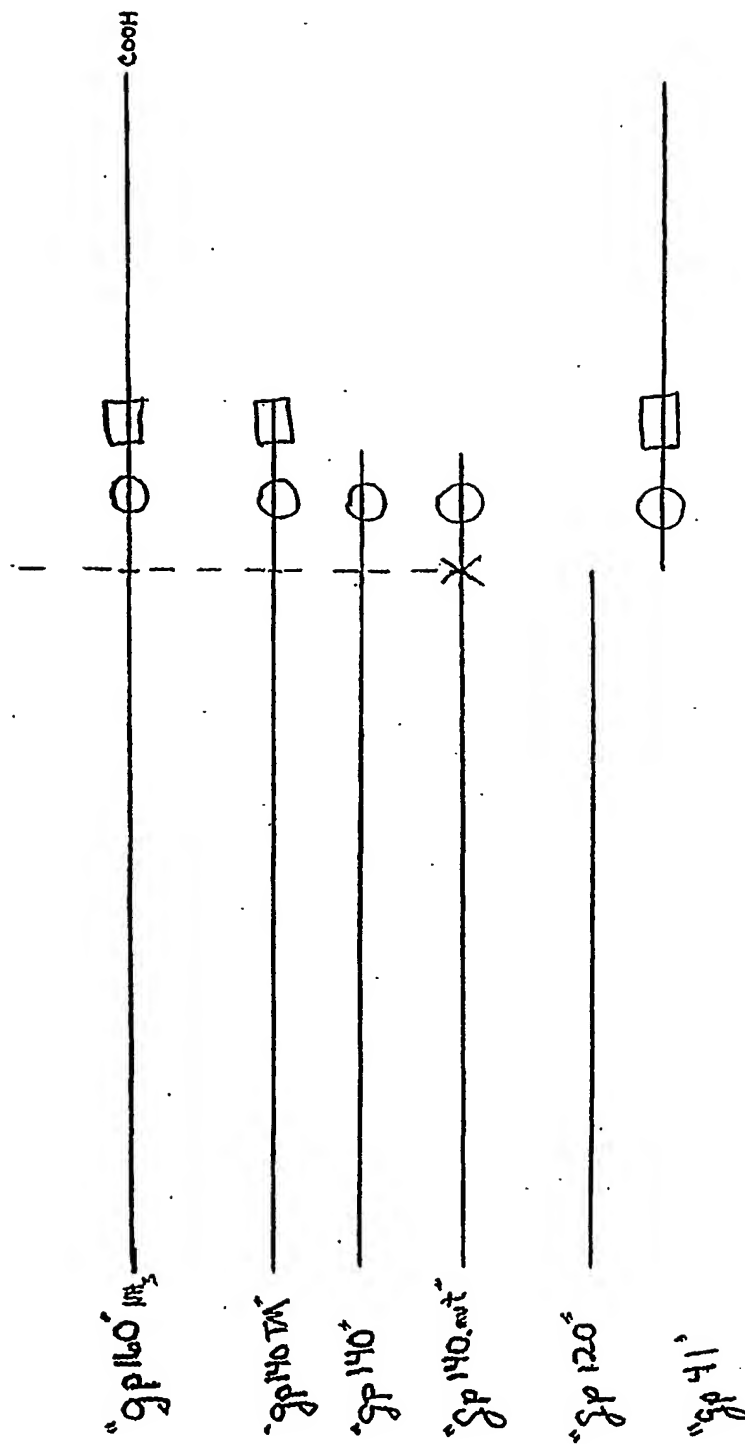
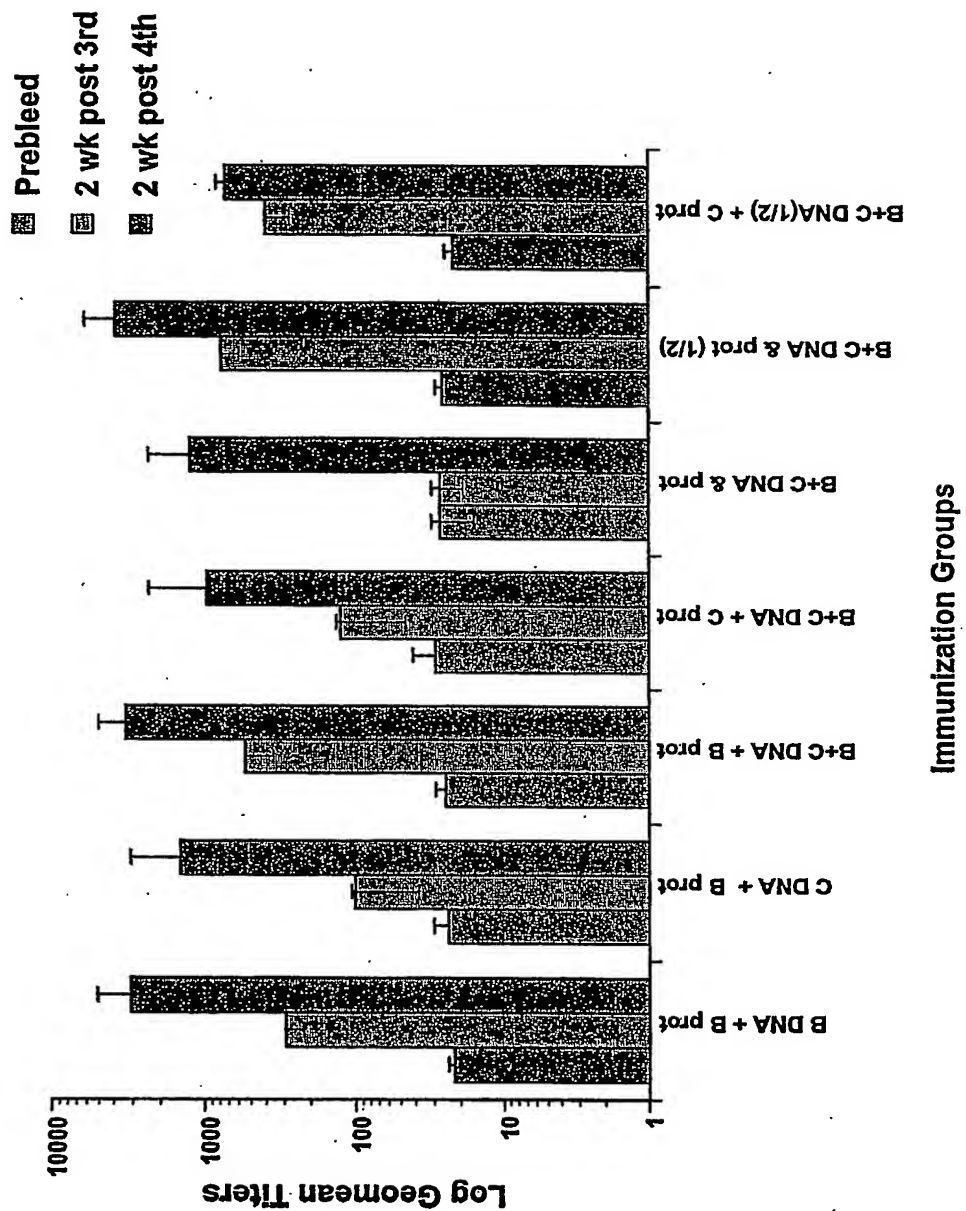
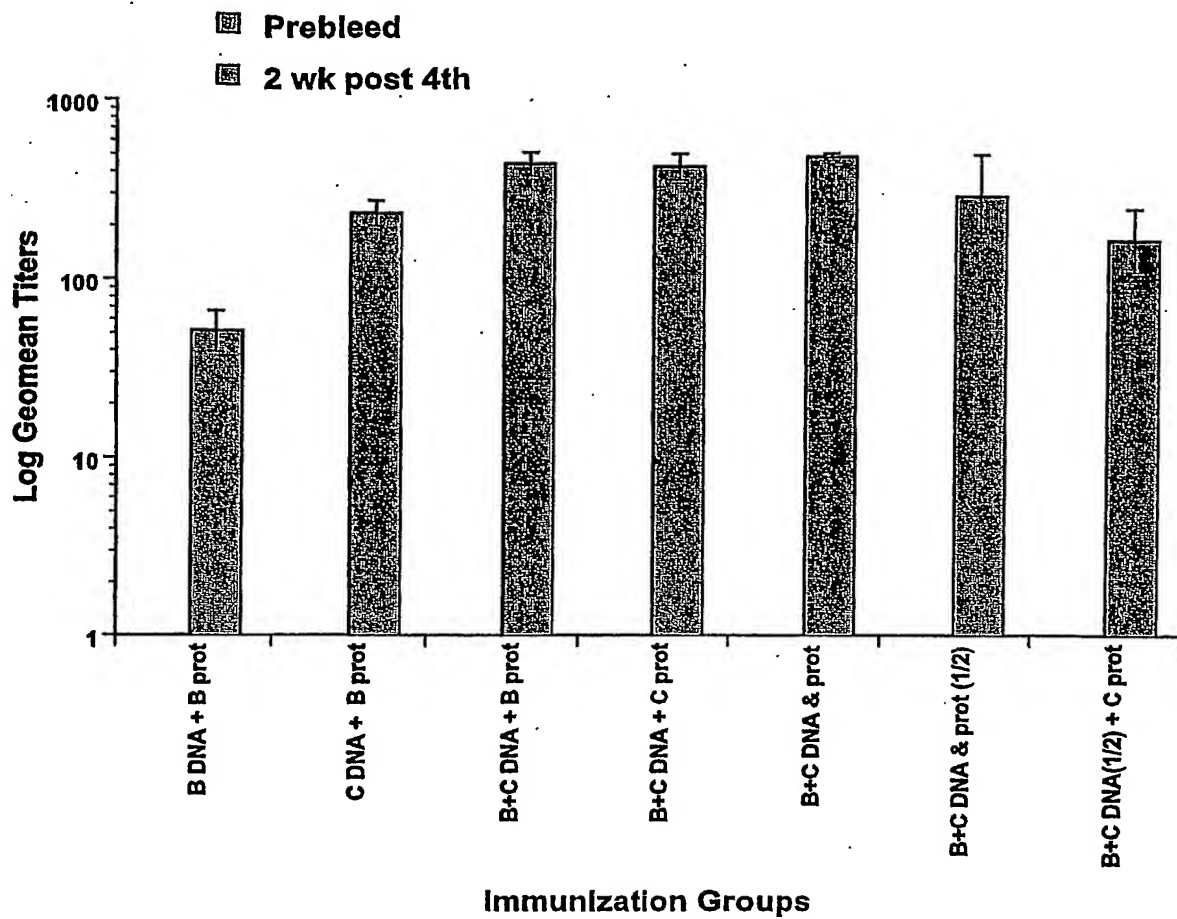


Figure 4



**Figure 5**

gp140.modSF162.delV2

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Figure 6

gp140.mut7.modSF162.delV2

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Figure 7

gp140mod.TV1.delV2

```

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961  ctgcagcagg tgatgaagaa gctgggcgag cacttcccca acaagacat ccagttcaag
1021  cccacgcgg gggcgacot ggagatoacc atgcacagot tcaactgocg cggogagttc
1081  ttctactgca acaccagcaa cctgttcaac agcaoctaco acagcaacaa cggcacotac
1141  aagtacaacg gcaacagcag cagcccoac accctgoagt gcaagatcaa gcagatcgtg
1201  cgcattgtggc agggcgtggg ccaggccacc tacgcccccc ccatcgccgg caacatcacc
1261  tgccgcagca acatcaocgg catcctgctg acccgagacg ggggttcaa caccaccaac
1321  aacaccgaga ccttccgccc cggcgggcgg gacatgcggc acaactggcg cagcgagctg
1381  tacaagtaca aggtggtgga gatcaagcc otgggcatcg cccccaccaa ggcoagcgc
1441  cgcgtggtgc agcgcgagaa gcgcgcgtg ggcacggcg ccgtgttctt ggggttctt
1501  ggcgcgcgcg gcagcaccat ggcgcgcgc agcatcacc tgaccgtgca ggcgcgcag
1561  ctgctgagcg gcacgtgca gcagcagagc aacctgctga aggcacatga ggccagcag
1621  cacatgctgc agctgaccgt gtggggcatc aagcagctgo agggcccgct gctggccatc
1681  gagcgctacc tgaaggacca gcagctgctg ggcactctgg getgcagcgg ccgctgctc
1741  tgcaccaocg ccgtgcoctg gaacagcagc tggagcaaca agagcgagaa ggacatctg
1801  gacaacatga cctggatgca gtgggaccgc gagatcagca actacaccgg cctgatctac
1861  aacctgctgg aggacagca gaaccagcag gagaagaacg agaaggacct gctggagctg
1921  gacaagtgga acaacctgtg gaactggttc gacatcagca actggccctg gtacatctaa
1981  ctogag

```

Figure 8

gp140mod.TV1.mut7.delV2

1 gaattcatgc gcgatgagg caaccagaag aactgcoago agtgggtgat ctgggggoatc  
 61 ctgggcttct ggatgtgat gatotgoaao acogaggaco tctgggtgao ogtgtactac  
 121 ggctgtcccg tctggogoga ogccaagacc accctgttct gogcoagoga ogcoaaggcc  
 181 tacgagaccg aggtgoaaoa ogtgtgggoc accoagocct gogtgocaoa cgaccccaac  
 241 cccaggaga tctgtctggg caactgtacc gagaacttca acatgtggaa gaacgacatg  
 301 gccgaccaga tgcagagga ogtgatcago ctgtgggaco agagocgtgaa gccotgctg  
 361 aagctgacco cctgtgctg gacctgaac tgoacogaca coaactgao oggcaaccgo  
 421 acogtgaccg goaacagcao caacaacacc aacoggoacc goacttataa catogaggag  
 481 atgaagaact gcagttcaa ogccggcgco gccogcctga toaactgaa caccagoccc  
 541 atoacccagg cctgcccacaa ggtgagcttc gaccccatcc ccatocacta ctgoccccc  
 601 gccggctacg ccatcctgaa gtgcaacaa aagacottca acggocaccg cccctgctac  
 661 aactgtagca cgtgcagtg caccocaggc atcaagcccg tggtagcaao coagctgctg  
 721 ctgaaggca gcttgccga ggagggcato atcatccga gcgagaacct gacogagaac  
 781 accaagacca tcatctgtca cctgaacgag agogtggaga tcaactgao cggcccaac  
 841 aacaacccc gcaagagcgt gogcatcggc cccggccagg ccttctacgo cacaacgao  
 901 gtgatoggca acatcogca gccccactgc aacatcagca cagaccgtg gaacaagacc  
 961 ctgcagcagg tgatgaagaa gctgggogag cacttccca acaagacct coagttcaag  
 1021 cccacggccg gcggogacct ggagatcac atgcacagct tcaactgcog oggogagttc  
 1081 ttctactgca acaccagca cctgttcaac agcacctacc acagcaacaa cggaacctac  
 1141 aagtaaacg gcaacagcag cagcccatc accctgcagt goaagatcaa gcagatcgtg  
 1201 cgcattgtggo agggcgtggg ccaggccaco tacgcccccc ccatogccgg caacatcaco  
 1261 tgcgcagca acatcacogg catcctgtg acccgcgacg goggttcaa caaccacaa  
 1321 aacaccgaga ccttcggccc ogcgggcggo gacatgcog acaactggog cagcagctg  
 1381 tacaagtaca aggtgggtga gatcaagccc ctgggcatcg cccccacaa gccatcago  
 1441 agcgtggtgc agagcgagaa gacgcccgtg ggcacggcg cctgttctct gggcttctg  
 1501 ggcgccggcg gcagcaccat ggcgccgccc agcatcacc tgacogtga gccocggcag  
 1561 ctgtgagcg gcatcgtgca gcagcagagc aactgctga aggcacatga gccocagcag  
 1621 caatgtctgc agctgacct gtggggcato aagcagctgc aggcggcgt gctggccato  
 1681 gacgctacc tgaaggacca gcagctgctg ggcattggg gctgcagogg ccgctgac  
 1741 tgaccaccc cgtgccctg gaacagcago tggagcaaca agagcgagaa ggacatctg  
 1801 gacaacatga cctggatgca gtgggaccgc gagatcagca actacacogg cctgatatao  
 1861 aacctgctgg aggcagcca gaaccagcag gagaagaac agaaggacct gctggagctg  
 1921 gacaagtgga acaacctgtg gaactgttc gacatcagca actggccctg gtacatatao  
 1981 ctogag

Figure 9



**FIGURE 10**  
gp160mod.Q23-17

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1  ATGCGCGTGA TGGGCATCCA GCGCAACTGC CAGCACCTGC TGACCTGGGG CATCATGATC
61  CTGGGCACCA TCATCTTCTG CAGCGCCGTG GAGAACCCTGT GGGTGACCGT GTACTACGGC
121 GTGCCCCGTGT GGC GCGACGC CGACAACCACC CTGTTCTGCG CCAGCGACGC CAAGGCCTAC
181 GAGACCGAGA AGCACAACGT GTGGGCCACC CACGCCTGCG TGCCCCACCGA CCCC AACC CC
241 CAGGAGATCC ACCTGGACAA CGTGACCGAG AAGTTCAACA TGTGGAAGAA CAACATGGTG
301 GAGCAGATGC ACACCGACAT CATCAGCCTG TGGGACCAGA GCCTGAAGCC CTGCGTGAAAG
361 CTGACCCCCC TGTGCGTGAC CCTGCACTGC ACCAACGTGA CCAGCGTGAA CACCACCGGC
421 GACCGCGAGG GCCTGAAGAA CTGCAGCTTC AACATGACCA CCGAGCTGCG CGACAAGCGC
481 CAGAAGGTGT ACAGCCTGTT CTACCGCCTG GACATCGTGC CCATCAACGA GAACCAGGGC
541 AGCGAGTACC GCCTGATCAA CTGCAACACC AGCGCCATCA CCCAGGCCTG CCCC AAGGTG
601 AGCTTCGAGC CCATCCCCAT CCACTACTGC ACCCCGCGCG GCTTCGCCAT CCTGAAAGTGC
661 AAGGACGAGG GCTTCAACGG CACCGGCCGTG TGCAAGAACG TGAGCACCCT CCAGTGACCC
721 CACGGCATCA AGCCCGTGGT GAGCACCCAG CTGCTGCTGA ACGGCAGCCT GGCCGAGAAAG
781 AACATCACCA TCCG CAGCGA GAACATCAQC AACAACGCCA AGATCATCAT CGTG CAGCTG
841 GTGCAGCCCG TGACCATCAA GTGCATCCGC CCCAACAACA ACACCCGCAA GAGCATCCGC
901 ATCGGCCCCG GCCAGGCCTT CTACGCCACC GCGGACATCA TCGGCGCAT CCGCCAGGCC
961 CACTGCAACG TGACCCG CAG CCGCTGGAAC AAGACCCTGC AGGAGGTGGC CGAGAAGCTG
1021 CGCACCTACT TCGGCAACAA GACCATCATC TTCGCCAACA GCAGCGGCGG CGACCTGGAG
1081 ATCACCACCC ACAGCTTCAA CTGCGGCGGC GAGTTCTTCT ACTGCAACAC CAGCGGCCCTG
1141 TTCAACAGCA CCTGGTACGT GAACAGCAC CCGAGCAGC CCGACAGCAC CCAGGAGAGC
1201 AACGACACCA TCACCCTGCC CTGCCGCATC AAGCAGATCA TCAACATGTG GCAGCGCGCC
1261 GGCCAGGCCA TGTACGCCCC CCCCATCCCC GCGGTGATCA AGTGCGAGAG CAACATCACC
1321 GGCCTGCTGC TGACCCGCGA CCGCGGCAAG GACAACAACG TGAACGAGAC CTTCCGCCCC
1381 GCGCGCGGCG ACATGCGCGA CAACTGGCGC AGCGAGCTGT ACAAGTACAA GGTGGTGGAG
1441 ATCGAGCCCC TGGGCGTGCG CCCCACCCGC GCCAAGCGCC GCGTGGTGGA GCGCGAGAAG
1501 CGCGCCGTGG GCATCGGCGC CGTGTTCTCTG GGCTTCCTGG GCGCCGCGCG CAGCACCATG
1561 GCGGCCACCA GCATCACCTT GACCGTGCAG GCCCGCCAGC TGCTGAGCGG CATCGTG CAG
1621 CAGCAGAACA ACCTGCTGCG CGCCATCGAG GCCCAGCAGC ACCTGCTGAA GCTGACCCTG
1681 TGGGGCATCA AGCAGCTGCA GGCCCGCGTG CTGGCCGTGG AGCGCTACCT GCGCGACCAG
1741 CAGCTGCTGG GCATCTGGGG CTGCAGCGGC AAGCTGATCT GCACCACCAA CGTGCCCTGG
1801 AACAGCAGCT GGAGCAACAA GAGCCTGGAC GAGATCTGGA ACAACATGAC CTGGCTGCAG
1861 TGGGACAAGG AGATCAACAA CTACCC CAG CTGATCTACC GCCTGATCGA GGAGAGCCAG
1921 AACCAGCAGG AGAAGAACGA GAAGGAGCTG CTGGAGCTGG ACAAGTGGGC CAACCTGTGG
1981 AGCTGGTTCC ACATCAGCAA CTGGCTGTGG TACATCAAGA TCTTCATCAT CATCGTGGGC
2041 GGCTTGATCG GCCTGCGCAT CGTGTTGCGC GTGCTGAGCG TGATCAACCG CGTGCGCCAG
2101 GGCTACAGCC CCCTGAGCTT CCAGACCCAC ACCCCCAACC CCCGCGGCCT GGACCGCCCC
2161 GAGCGCATCG AGGAGGAGGA CCGCGAGCAG GGCGCGGCC GCAGCATCCG CCTGGTGAGC
2221 GGCTTCCTGG CCCTGGCCTG GGACGACCTG CGCAGCCTGT GCCTGTT CAG CTACCACEGC
2281 CTGCGCGACT TCATCCTGAT CGCCGCCCGC ACCGTGGAGC TGCTGGGCCA CAGCAGCCTG
2341 AAGGGCCTGC GCCTGGGCTG GGAGGGCATC AAGTACCTGT GGAACCTGCT GAGCTACTGG
2401 GGCCGCGAGC TGAAGATCAG CGCCATCAAC CTGGTGACA CCATCGCCAT CGCCGTGGCC
2461 GGCTGGACCG ACCGCGTGAT CGAGATCGCC CAGCGCATCG GCCGCGCCAT CCTGCACATC
2521 CCCGTGCGCA TCCGCCAGGG CCTGGAGCGC GCCCTGCTGT AA

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**FIGURE 11**

gp160mod.98UA0116

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1 ATGAAGGCCC GCGGCATGCA GCGCAACTAC CAGCACCTGT GCGGCTGGGG CACCATGCTG
61 TTCTGGATGA TCATCATGTG CAAGGCCGCC GAGAACCCTGT GGGTGACCGT GTACTACGGC
121 GTGCCCCGTGT GCGCGGACGC CGAGATCACC CTGTTCTGCG CCAGCGACGC CAAGGCCTAC
181 GACAAGGAGG TGCACAACGT GTGGGCCACC CACGCCCTGCG TGCCCAACGA CCCCAGCCCC
241 CAGGAGATCA TCCTGGAGAA CGTGACCGAG AAGTTCAACA TGTGGAAGAA CAACATGGTG
301 GAGCAGATGC AGACCGACAT CATCAGCCTG TGGGACCAGA GCCTGAAGCC CTGCGTGAAG
361 CTGACCCCCC TGTGCGTGAC CCTGAAGTGC GCCGGCCCCA GCAGCAACAA CAGCAACGTG
421 AACAGCAACA GCAACGACAA CTGGAGCGAG GAGATGAAGA ACTGCAGCTT CAACATGACC
481 ACCGAGCTGC GCGACAAGCG CAAGACCGTG CACAGCCTGT TCTACAAGCT GGACATCGTG
541 AGCACCAGGCA GCAACGACAG CCGCCAGTAC CGCCTGATCA ACTGCAACAC CAGCGCCATG
601 ACCCAGGCCT GCCCAAGGT GACCTTCGAG CCCATCCCCA TCCACTACTG CGCCCCCGCC
661 GGCTTCGCCA TCCTGAAGTG CAAGGACACC AACTTCACCG GCACCGGCCC CTGCAAGGAC
721 GTGAGCACCG TGCAGTGAC CCACGGCACC AAGCCCGTGG TGAGCACCCA GCTGCTGCTG
781 AACGGCAGCC TGGCCGAGAA GGAGGTGATG ATCCGAGCG AGAACATCAC CGACAACGGC
841 AAGATCATCA TCGTGAGCT GACCGAGCCC GTGAACATCA CCCGCATCCG CCCCAGCGAG
901 AACAAGCGCA CCAGCATCCG CATCGGCCCC GGCCAGACCT TCTAGCCAC CGGCGACGTG
961 ATCGGCGACA TCCGCAAGGC CTACTGCAAC GTGAGCCGCG CCGCTGGAA CAGCACCTG
1021 CAGAAGATCA GCACCCAGCT GCGCCAGTAC TTCAACAACA AGACCATCAT CTTCAAGAAC
1081 AGCAGCGGCG GCGACCTGGA GGTGACCACC CACAGCTTCA ACTGCGGCGG CGAGTTCTTC
1141 TACTGCAACA CCACCGACCT GTTCAACAGC ACCTGGAACG AGCAGGCCCC CGTGACCAAC
1201 AGCACCATGG CCAACGGCAC CATCACCTG CCGTGGCGCA TCAAGCAGAT CATCAACATG
1261 TGGCAGCGCG TGGGCCAGGC CATGTACGCC CCCCCATCG AGGGCAACAT CGGCTGCGAG
1321 AGCAACATCA CCGGCTGCT GCTGACCCGC GACGGCGGCA GCGGCGCCAA CAGCAGCAAG
1381 GAGACCTACC GCCCATCGG CGGCAACATG CGCGCAACT GCGCAGCGA GCTGTACAAG
1441 TACAAGGTGG TGAAGATCGA GCCATCGGC GTGGCCCCCA CCAAGGCCAA GCGCCGCGTG
1501 GTGGAGCGCG AGAAGCGCGC CATCGGCCCTG GCGCGCCCT TCCTGGGCTT CCTGGGCGCC
1561 GCGGCGAGCA CCATGGGCGC CGCCAGCATG ACCCTGACCG TGCAGGCCCG CCAGCTGCTG
1621 AGCGGCATCG TGCAGCAGCA GAGCAACCTG CTGCGCGCCA TCGAGGCCCA GCAGCACCTG
1681 CTGAAGCTGA CCGTGTGGGG CATCAAGCAG CTGCAGGCCC GCGTGCTGGC CGTGGAGCGC
1741 TACCTGAAGG ACCAGCAGCT GCTGGGCATC TGGGGCTGCA GCGGCAAGCT GATCTGCACC
1801 ACCAACGTGC CCTGGAACAG CAGCTGGAGC AACAAAGACC AGAGCGAGAT CTGGGGCAAC
1861 ATGACCTGGA TGCAGTGGGA CCGCGAGGTG ATCAACTACA CCAACATCAT CTACGACCTG
1921 ATCGAGGAGA GCCAGAACCA GCAGGAGAAG AACGAGCAGG ACCTGCTGGC CCTGGACAAG
1981 TGGGCCAGCC TGTGGAGCTG GTTCGACATC AGCAACTGGC TGTGGTACAT CAAGATCTTC
2041 ATCATCATCG TGGGCGGCCT GATCGGCCCTG CGCATCGTGT TCGCCGTGCT GAGCATCATC
2101 AACCAGCGCG GCCAGGGCTA CAGCCCCCTG AGCCTGCAGA CCCTGACCCC CCACCCCGAG
2161 GGCCCCGACC GCCCCGGCCG CATCAAGGAG GAGGGCGGCG AGCAGGACCG CGACCGCAGC
2221 ATCCGCCTGG TGAGCGGCTT CCTGGCCCTG GCCTGGGACG ACCTGCGCAG CCTGTGCCTG
2281 TTCAGCTACC GCGCCTGCG CGACTTCATC AGCATCGCCG CCCGCACCGT GGAGCTGCTG
2341 GGCCGAGCA GCCTGAAGGG CCTGCGCCTG GGCTGGGAGG GCCTGAAGTA CCTGGGCAAC
2401 CTGCTGGGCT ACCGCGGCCA GGAGCTGAAG AGCAGCGCCA TCAACCTGAT CGACACCATC
2461 GCCATCGCCG TGGCCGGCTG GACCGACCGC GTGATCGAGA TCGGCCAGCG CTTCTGCCCC
2521 GCCATCCGCA ACATCCCCCG CCGCATCCGC CAGGGCGCCG AGCGCGCCCT GCAGTAA

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**FIGURE 12**gp160<sub>mod</sub>.SE8538

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1  ATGCGCGTGA AGGGCATCCA GCGCAACAGC CAGCACCTGC TCGCTGGGG CACCATGATC
61 CTGGGCATGA TCATCATCTG CAGCACCGCC GACAAGCTGT GGTGACCGT GTACTACGGC
121 GTGCCCCTGT GGAAGGACGC CGAGACCACC CTGTTCTGCG CCAGCGACGC CAAGGCCCTAC
181 GACACCGAGG TGCACAACGT GTGGGCCACC CACGCCCTGCG TGCCCACCGA CCCCACCC.
241 CAGGAGCTGC ACCTGGCCAA CGTGACCGAG GAGTTCAACA TGTGGAAGAA CAGCATGGTG
301 GAGCAGATGC ACACCGACAT CATCAGCCTG TGGGACCAGA GCCTGATCCC CTGCGTGAAG
361 CTGACCCCCC TGTGCGTGAC CCTGGAGTGC AACGACTACA ACTACAACGT GACCAACAGC
421 AGCCACAGCT ACAACGTGAC CAACATGCAG GAGATGAAGA ACTGCAGCTT CAACGTGACC
481 ACCGAGCTGC GCGACAAGCG CCAGAAGGTG ACCAGCCTGT TCTACAAGCT GGACGTGGTG
541 CCCATCGCGC GCAACGACAC CAACAGCACC CAGTACCGCC TGATCAACTG CAACACCAGC
601 GCCATCACCC AGGCCTGCCA CAAGGTGACC TTCGAGCCCA TCCCATCCA CTACTGCGCC
661 CCCGCCGGCT TCGCCATCCT GAAGTGCCGC GAGGAGAAGT TCAACGGCCT CGACCGCTGC
721 AAGAACGTGA GCACCGTGCA GTGCACCCAC GGCATCAAGC CCGTGGTGAG CACCCAGCTG
781 CTGCTGAACG GCAGCCTGGC CCGCGAGAAG GTGATGATCC GCAGCGAGAA CATCACCAC
841 AACGTGAAGA ACATCATCGT GCAGCTGAAG GAGCCCGTGG AGATCAACTG CACCCGCCCC
901 GGCAACAACA CCCGCAAGAG CATCCGCATC GGCCCCGGCC AGGCCTTCTA CGCCACCGGC
961 GAGGTGATCG GCGACATCCG CCAGGCCAC TGCAACGTGA GCCGCGCCAA GTGGAACAAG
1021 ACCCTGCACG AGGTGGCCAA GCAGCTGCGC ACCTACTTCA ACAACAAGAC CATCATCTTC
1081 ACCAACAGCA GCGGCGGCGA CCTGGAGATC ACCACCCACA CCGTGAATG CCGGCGCGAG
1141 TTCTTCTACT GCAACACCAG CGGCCTGTTC AACAGCACCT GGAGCAGCAA CGCCACCGAG
1201 CCCATGAGCA ACAGCACCAG GAGCAACGAC ACCATCACCC TGCAGTGCCG CATCCGCCAG
1261 ATCATCAACA TGTGGCAGCG CGCCGGCAAG GCCATCTACG CCCCCCCAT CCCCGGCATC
1321 ATCAAGTGCG TGAGCAACAT CACCGGCCTG ATCCTGACCC GCGAGGCGCG CAGCAACAAC
1381 AGCAACCAAG AGACCTTCCG CCCCAGCGGC GCGACATGC GCGACAAGTG CCGCAGCGAG
1441 CTGTACAAGT ACAAGGTGGT GAAGATCGAG CCCCTGGGCG TGGCCCCAC CAAGGCCAAG
1501 CGCCGCGTGG TGGAGCGCGA GAAGCGCGCC ATCGGCATCG GCGCCGTGTT CATCGGCTTC
1561 CTGGGCGCCG CCGGCAGCAC CATGGGCGCC GCCAGCATCA CCCTGACCGT GCAGGCCCGC
1621 CAGCTGCTGA GCGGCATCGT GCAGCAGCAG AGCAACCTGC TGCAGCGCAT CGAGGCCAG
1681 CAGCACCTGC TGAAGCTGAC CGTGTGGGGC ATCAAGCAGC TGCAGGCCCG CGTGTGGCC
1741 GTGGAGCGCT ACCTGAAGGA CCAGCAGCTG CTGGGCATCT GGGGCTGCAG CGGCAAGCTG
1801 ATCTGCACCA CCAACGTGCC CTGGAACAGC AGCTGGAGCA ACAAGAGCCA GAGCGAGATC
1861 TGGGACAACA TGACCTGGCT GCAGTGGGAC AAGGAGATCA GCAACTACAC CCAGACCATC
1921 TACCGCTGA TCGAGGAGAG CCAGAACCAG CAGGAGAAGA ACGAGCAGGA CCTGCTGGCC
1981 CTGGACAAGT GGGCCAGCCT GTGGAAGTGG TTCGACATCA GCCGCTGGCT GTGTACATC
2041 CGCATCTTCA TCATGATCGT GGGCGGCTG ATCGGCCTGC GCATCGTGTT CGCCGTGCTG
2101 AGCGTGATCA ACCGCGTGC CGAGGGCTAC AGCCCCCTGA GCTTCCAGAT CCACACCC
2161 AACCCGCGCG ACCTGGACCG CCCCAGCGGC ATCGAGGAGG AGGGCGGCGA GCAGGACCGC
2221 GGCCGAGCA TCCGCTGGT GAGCGGCTTC CTGGCCCTGG CCTGGGACGA CCTGCGCAGC
2281 CTGTGCCTGT TCAGCTACCA CCGCTGCGC GACTTCATCC TGATCGCCGC CCGCACCCTG
2341 GAGCTGCTGG GCCAGCGCGG CTGGGAGGGC CTGAAGTACC TGTGGAACCT GCTGGTGTAC
2401 TGGATCCGCG AGCTGAAGAT CAGCGCCATC AGCCTGCTGG ACACCATCGC CATCGCCGTG
2461 GCCGCTGGA CCGACCGCGT GATCGAGCTG GGCCAGCGCC TGTGCCGCGC CATCCTGCAC
2521 ATCCCGTGC GCATCCGCCA GGGCTTCGAG CGCGCCCTGC TGTA

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**FIGURE 13**

gp160mod.UG031

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1 ATGCGCGTGC GCGGCATCCA GACCAGCTGG CAGAACCTGT GCGCGTGGGG CACCATGATC
61 CTGGGCATGC TGATGATCTA CAGCGCCGCC GAGAACCTGT GGGTGACCGT GTACTACGGC
121 GTGCCCCTGT GGAAGGACGC CGAGACCACC CTGTTCTGCG CCAGCGACGC CAAGGCCTAC
181 GACACCGAGG TGCACAACGT GTGGGCCACC CACGCCCTGCG TGCCCAACGA CCCCACCCC
241 CAGGAGATCC ACCTGGAGAA CGTGACCGAG GACTTCAACA TGTGGAAGAA CAACATGTTG
301 GAGCAGATGC ACACCGACAT CATCAGCCTG TGGGACCAGA GCCTGAAGCC CTGCGTGGAG
361 CTGACCCCCC TGTGCGTGAC CTTGGACTGC CTGAACGCCA CCTGAACGC CACCGCCCCC
421 AACGTGACCA ACGACATGGA GGGCGAGATG AAGAACTGCA GCTACAACAT CACCACCGAG
481 CTGAAGGACA AGAAGCAGCA GGTGTACAGC CTGTTCTACA AGCTGGACGT GGTGCAGATC
541 AACGAGAAGA ACAAGACCAA CAAGTACCGC CTGATCAACT GCAACACCAG CGCCATCACC
601 CAGGCCTGCC CCAAGGTGAG CTTGAGCCCT ATCCCATCC ACTACTGCGC CCCCGCCGCG
661 TTCGCCATCC TGAAGTGCAA GGACACCGAG TTCAACGGCA CCGGCCCCCTG CAAGAACGTG
721 AGCACCGTGC AGTGACCCCA CGGCATCCGC CCCGTGATCA GCACCCAGCT GCTGCTGAAC
781 GGCAGCCTGG CCGAGGGCGG CATCCAGATC CGCAGCGAGA ACATCACCAA CAACGCCAAG
841 ACCATCATCG TGCAGCTGGA CAAGGCCGTG AAGATCAACT GCACCCGCCG CAACAACAAC
901 ACCCGCAAGA GCGTGCGCAT CCGCCCCGGC CAGGCCTTCT ACGCCACCGG CGACATCATC
961 GCGGACATCC GCCAGGCCCCA CTGCAACGTG AGCCGCGCCA AGTGAACGA GACCTGCGC
1021 GGCATCGCCA AGAAGCTGAG CGAGCACTTC AAGAACAAGA TCATCATCTT CGAGAAGAGC
1081 AGCGGCGGCG ACATCGAGAT CACCAACCAC AGCTTCAACT GCGGCGGCGA GTTCTTCTAC
1141 TGCAACACCA GCGGCCTGTT CAACGGCACC TGGAAGCCCA ACAGCACCGA GAGCAACAAC
1201 ACCACCCCCA ACGACACCAT CACCTGACC TGCCGCATCA AGCAGATCAT CAACATGTGG
1261 CAGAAGGTGG GCCAGGCCAT GTACGCCCCC CCCATCCAGG GCGTGATCCG CTGCGAGAGC
1321 AACATCACCG GCCTGCTGCT GACCCGCGAC GCGGCGATCA ACAGCATCA CGAGACCTTC
1381 CGCCCCGGCG GCGGCAACAT GCGCGACAAC TGGCGCAGCG AGCTGTACAA GTACAAGGTG
1441 GTGAAGATCG AGCCCCCTGGG CGTGGCCCCC AGCCGCGCCA AGCGCCGCGT GGTGGAGCGC
1501 GAGAAGCGCG CCGTGGGCAT CCGCGCCGTG TTCTGGGCT TCCTGGGCGC CGCCGCGAGC
1561 ACCATGGGCG CCGCCAGCAT CACCTGACC GCCAGGCCG GCCAGTGTG GAGCGGCATC
1621 GTGCAGCAGC AGAGCAACCT GCTGCGCGCC ATCAAGGCCC AGCAGCACAT GCTGAAGCTG
1681 ACCGTGTGGG GCATCAAGCA GCTGCAAGGC CGCGTGCTGG CCGTGGAGCG CTACCTGAAG
1741 GACCAGCAGC TGCTGGGCAT CTGGGGCTGC AGCGGCAAGC TGATCTGCAC CACCAACGTG
1801 CCTGGAACA GCAGCTGGAG CAACAAGAGC ATGAACGAGA TCTGGGACAA CATGACCTGG
1861 CTGCAGTGGG AGAAGGAGAT CAGCAACTAC ACCCAGCTGA TCTACAACCT GATCAGGAG
1921 AGCCAGAACC AGCAGGAGAA GAACGAGCAG GACCTGCTGG CCCTGGACAA GTGGGCCAGC
1981 CTGTGGAAC TGTTCGACAT CAGCCGCTGG CTGTGGTACA TCAAGATCTT CATCATGATC
2041 GTGGGCGGCC TGATCGGCCT GCGCATCGTG TTCGCCGTGC TGAGCGTGAT CAACCGCGTG
2101 CGCCAGGGCT ACAGCCCCCT GAGCTTCCAG ATCCGCACCC CCAACCCCGA GGAGCCCGAC
2161 CGCCTGGGCC GCATCGGCCA GGAGGGCGGC GAGCAGGACC GCGACCGCAG CATCCGCTG
2221 GTGAGCGGCT TCCTGGCCCT GGCCTGGGAC GACCTGCGCA GCCTGTGCT GTTCAGCTAC
2281 CACCGCCTGC GCGACTTCAT CAGCATCGCC GCCCGCACCG TGGAGCTGCT GGGCCACAGC
2341 AGCCTGAAGG GCCTGCGCCT GGGCTGGGAG GGCCTGAAGT ACCTGTGGAA CCTGCTGCTG
2401 TACTGGGGCC TGGAGCTGAA GACCAGCGCC GTGAACCTGG TGGACACCAT CGCCATCGCC
2461 GTGGCCGGCT GGACCGACCG CGTGATCGAG ATCGGCCAGC GCATCTTCCG CGCCATCCTG
2521 AACATCCCCC GCCGCATCCG CCAGGGCCTG GAGCGCGGCC TGCTGTAA

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**FIGURE 14**

gp160mod.92UG001

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1  ATGCGCGTGC GCGAGATCGA GCGCAACTAC CTGTGCCTGT GCGCGCTGGG CATCATGCTG
61 CTGGGCGATGC TGATGACCTA CAGCGTGGCC GAGAAGAAGT GGGTGACCGT GTACTACGGC
121 GTGCCCCGTGT GGAAGGAGGC CACCACCACC CTGTTCTGCG CCAGCGACGC CAAGAGCTAC
181 AAGACCGAGG TGCACAACAT CTGGGCCACC CACGCCTGCG TGCCCACCGA CCCCACCCCC
241 CGCGAGATCG AGCTGGAGAA CGTGACCGAG AACTTCAACA TGTGGAAGAA CAACATGGTG
301 GAGCAGATGC ACGAGGACAT CATCAGCCTG TGGGACCAGA GCCTGAAGCC CTGCGTGAAG
361 CTGACCCCCC TGTGCGTGAC CCTGAACTGC ACCGACGCCC GCCGCAACGA GACCCGCAAC
421 AACATCACCG GCATGGAGAA CAACGACCAG ATCGAGATGA AGAACTGCAG CTTCAACATC
481 ACCACCAAGC TGATCGACAA GAAGAAGCAG GTGCACGCCC TGTTCACCG CCTGGACGTG
541 GTGCAGATCG ACAACGACAC CAGCAACAGC AACTACAGCA ACTACCGCCT GATCAACTGC
601 AACACCAGCG CCATCACCCA GGCCTGCCCC AAGGTGACCT TCGAGCCCAT CCCCATCCAC
661 TACTGCGCCC CCGCCGGCTT CGCCATCCTG AAGTGCCGCG ACAAGAAGTT CAACGGCACC
721 GGCCCCCTGCA AGAACGTGAG CACCGTGCAG TGCACCCACG GCATCCGCCC CGTGGTGAGC
781 ACCCATCAAGC AGATCATCAA CAGCCTGGCC GAGGAGGAGA TCATCATCCG CAGCGAGAAC
841 CTGACCAACA ACGCCAAGAC CCTGATCGTG CAGCTGAACG AGAGCGTGGA GATCAACTGC
901 ACCCGCCCCCT ACTACAACCA GATCGGCCAG CGCACCAGCA TCGGCCAGGG CCAGGCCCTG
961 TACACCACCC GCGTGACCGG CGACATCCGC AAGGCCCTACT GCAACATCAG CAAGGCCCGG
1021 TGGACAAGA CCCTGCAGCA GGTGGCCAG AAGCTGGGCG ACCTGTTCAA CCAGACCACC
1081 ATCATCTTCA AGCCCAGCAG CGGCGGCGAC CCCGAGATCA CCACCCACAG CTTCAACTGC
1141 GCGGCGCGAGT TCTTCTACTG CAACACCAGC AAGCTGTTCA ACAGCGCCTG GAACGACAGC
1201 ACCTGGAACA TCGGCAACAA CAACACCAGG AGCGACAACG AGACCATCAT CATCCCCTGC
1261 CGCATCAAGC AGATCATCAA CATGTGGCAG GCGTGGGCA AGGCCATGTA CGCCCCCCCC
1321 ATCGAGGGCT GGATCAACTG CGCCAGCAAC ATCACCAGCC TGCTGCTGGT GCGCGACGGC
1381 GCGGCGGCCA ACGACAGCCA GAACGAGACC TTCCGCCCCC AGGGCGGCGA CATGCGCGAC
1441 AACTGGCGCA GCGAGCTGTA CAAGTACAAG GTGGTGAAGA TCGAGCCCCC GGGCATCGCC
1501 CCCACCAAGG CCAAGCGCCG CGTGGTGGAG CGCGAGAAGC GCGCCATCGG CCTGGGCGCC
1561 ATGTTCTTGG GCTTCTTGGG CGCCGCCGGC AGCACCATGG GCGCCGCCAG CTGACCCCTG
1621 ACCGTGCAGG CCCGCCAGCT GCTGAGCGGC ATCGTGCAGC ACCAGAACAA CCTGCTGATG
1681 GCCATCGAGG CCCAGCAGCA COTGCTGCAG CTGACCGTGT GGGGCATCAA GCAGCTGCAG
1741 GCCCGCATCC TGGCCGTGGA GCGCTACCTG CAGGACCAGC AGCTGCTGGG CAGCTGGGGC
1801 TGCAGCGGCC GCCACATCTG CACCACCACC GTGCCCTGGA ACAGCAGCTG GAGCAACAAG
1861 AGCATCGACG ACATCTGGAA CAACATGACC TGGATGGAGT GGGAGAAGGA GATCGACAAC
1921 TACACCGGCG TGATCTACCG CCTGATCGAG GAGAGCCAGA CCCAGCAGGA GAAGAACGAG
1981 CAGGAGCTGC TGCAGCTGGA CAAGTGGGCC AGCCTGTGGA ACTGGTTCAG CATCACCAG
2041 TGGCTGTGGT ACATCAAGAT CTTTCATCATG ATCGTGGGCG GCCTGATCGG CCTGCGCATC
2101 GTGTTACCG TGCTGAGCCT GGTGAACCGC GTGCCCCAGG GCTACAGCCC CCTGAGCTTC
2161 CAGACCCTGT TCCCCGCCCC CCGCGGCCCC GACCGCCCCG AGGAGATCGA GGAGGGCGGC
2221 GCGGAGCAGG GCCCGGGCCG CAGCACCCGC CTGGTGAACG GCTTCAGCAC CCTGATCTGG
2281 GACGACCTGC GCAACCTGTG CCTGTTCAGC TACCACCGCC TGCGCGACCT GATCCTGATC
2341 GCCACCCGCA TCGTGGAGCT GCTGGGCGGC CGCGGCTGGG AGGCCATCAA GTACCTGTGG
2401 AACCTGCTGC AGTACTGGAG CCAGGAGCTG AAGACCAGCG CCATCAGCCT GTTCAACGCC
2461 ACCGCCGTGG CCGTGGCCGA GGGCACCGAC CGCGTGATCG AGGTGGTGCA GCGCTTCTTC
2521 CGCGGCATCC TGAACGTGCC CACCCGCATC CGCCAGGGCC TGGAGCGCGC CTGCTGTAA

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**FIGURE 15**

gp160mod.94UG114

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1  ATGCGCGTGC GCGAGACCAA GCGCAACTAC CAGCACCTGT GGAAGTGGGG CACCATGCTG
61 CTGGGCATGC TGATGATCTG CAGCGTGACC GGCAAGAGCT GGGTGACCGT GTACTACGGC
121 GTGCCCCTGT GGAAGGAGGC CACCACCACC CTGTTCTQCG CCAGCGACGC CAAGGCCTAC
181 AAGGCCGAGG CCCACAACAT CTGGGCCACC CACGCTGCG TGCCCACCGA CCCCACCCC
241 CAGGAGATCA AGCTGGAGAA CGTGACCGAG AACTTCAACA TGTGGAAGAA CAACATGGTG
301 GAGCAGATGC ACGAGGACAT CATCAGCCTG TGGGACCAGA GCCTGAAGCC CTGCGTGAAG
361 CTGACCCCCC TGTGCGTGAC CCTGAACTGC ACCAACTGGG TGACCGACAC CACCAACACC
421 ACGGCATGG CCAACTGCAG CTTCAACATC ACCACCGAGA TCGCGACAA GAAGAAGCAG
481 GTGCAGGCCC TGTCTACAA GCTGGACGTG GTGAAGATCA ACGACAACGA CAGCGACAAC
541 ACCAGTACC GCCTGATCAA CTGCAACACC AGCGCCATCA CCCAGGCCGT CCCCAGATG
601 ACCTTCGAGC CCATCCCCAT CCACTACTGC GCCCCCGCCG GCTTCGCCAT CCTGAAGTGC
661 AACGAGAAGA AGTTCAACGG CACCGGCCCG TGCAGAAGC TGAGCACCCG GCAGTGCACC
721 CACGGCATCA AGCCCGTGGT GAGCACCCAG CTGCTGTGTA ACGGCAGCCT GGCCGAGGAG
781 GAGATCATCA TCCGCAGCGA GAACCTGACC AACACGCCA AGATCATCAT CGTGCACTG
841 AACGAGAGCG TGCCCATCAA CTGCATCCGC CCCACAACA ACACCCGCCA GAGCACCCGC
901 ATCGGCCCGG GCCAGGCCCT GTCACCAACC AAGGTGATCG GCGACATCG CCAGGCCAC
961 TGCAACATCA GCGGCGCCGG CTGGAACAAG ACCCTGCAGC AGGTGGCCGA GAAGCTGGGC
1021 AACCTGTGTA ACCAGACCAC CATCATCTTC AAGCCAGCA GCGGCGCGCA CCCCAGATC
1081 ACCACCACA GCTTCAACTG CGGCGGCGAG TTCTTCTACT GCAACACCAC CCGCTGTTC
1141 AACGACACCT GGAAGCGCAA CACAGCGAG TGGCGCAGCG ACAACACCCT CGACGAGACC
1201 ATCACCTGCG AGTGCCGCAT CAAGCAGATC ATCAACATGT GGCAGGAGGT GGGCAAGGCC
1261 ATGTACGCC CCCCATCGA GGGCTTCATC AACTGCAGCA GCAACATCAC CGGCCTGCTG
1321 CTGACCCGCG ACGGCGGCGC CATCAACAGC AGCCAGAAGC AGACCTTCCG CCCCAGCGGC
1381 GCGGACATGC GCAACAAC TGCGAGCGAG CTGTACAAGT ACAAGGTGGT GAAGCTGGAG
1441 CCCATCGGCC TGCCCCCAC CGCCGCCAAG CGCCGCGTGG TGGAGCGCGA GAAGCGCGCC
1501 ATCGGCCCTG GCGCCCTGTT CCTGGGCTTC CTGGGCACCG CCGGCAGCAC CATGGGCGCC
1561 GTGAGCCTGA CCTGACCGT GCAGGCCCGC CAGGTGTGTA GCGGCATCGT GCAGCAGCAG
1621 AACAACTGC TGCGCGCCAT CGAGGCCCGC CAGCACCTGC TGCACTGAC CGTGTGGGGC
1681 ATCAAGCAGC TGCAAGCCCG CATCCTGGCC GTGGAGAGCT ACCTGAAGGA CCAGCAGCTG
1741 CTGGGCATCT GGGCTGCGAG CGGCAAGCAC ATCTGCACCA CCAACGTGCC CTGGAACAGC
1801 AGCTGGAGCA ACCGAGCGT GGACGAGATC TGGAAACAACA TGACCTGGAT GGAGTGGGAG
1861 CGCGAGATCG ACAACTACAC CGAGCTGGTG TACAGCCTGC TGGAGGTGAG CCAGATCCAG
1921 CAGGAGAAGA ACGAGCAGGA GCTGCTGAAG CTGGACACCT GGGCCAGCCT GTGGAAGTGG
1981 TTCAGCATCA CCAAGTGGCT GTGGTACATC AAGATCTTCA TCATGATCGT GGGCGGCTG
2041 ATCGGCCCTG GCATCGTGTT CGCCGTGCTG AGCGTGGTGA ACCGCGTGGC CCAGGGCTAC
2101 AGCCCCCTGA GCTTCCAGAC CTTGCTGCC CCCCCCGCG AGCCCGACCG CCCCAGGGC
2161 ATCGAGGAGG AGGGCGGCGA GCGCGACCGC GGCCGCAGCA TCCGCTGGT GAACGGCTG
2221 AGCGCCCTGA TCTGGGACGA CCTGCGCAAC CTGTGCCTGT TCAGCTACCA CCGCTGCGC
2281 GACCTGATCC TGATCGCCGC CCGCATCGTG GAGCTGCTGG GCCCGCGCG CTGGGAGGCC
2341 ATCAAGTACC TGTGGAACCT GCTGCAGTAC TGGATCCAGG AGCTGAAGAA CAGCGCCGTG
2401 AGCCTGTTCA ACACCATCGC CATCGCCGTG GCCGAGGGCA CCGACCGCG CATCGAGCTG
2461 GTGCAGCGCG CCGTGCAGCG CATCCTGAAC ATCCCCTGCG GCATCCGCCA GGGCTGGAG
2521 CGCGCCCTGC TGTA

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**FIGURE 16**

gp160mod:ELI

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1 ATGCGCGCCC GCGGCATCGA GCGCAACTGC CAGAACTGGT GGAAGTGGGG CATCATGCTG
61 CTGGGCATCC TGATGACCTG CAGCGCCGCC GACAACCTGT GGGTGACCGT GTACTACGGC
121 GTGCCCGTGT GGAAGGAGGC CACCACCACC CTGTTCTGCG CCAGCGACGC CAAGAGCTAC
181 GAGACCGAGG CCCACAACAT CTGGGCCACC CACGCTGCG TGCCACCGCA CCCCACCCC
241 CAGGAGATCG CCCTGGAGAA CGTGACCGAG AACTTCAACA TGTGGAAGAA CAACATGGTG
301 GAGCAGATGC ACGAGGACAT CATCAGCCTG TGGGACCAGA GCCTGAAGCC CTGCGTGAAG
361 CTGACCCCCC TGTGCGTGAC CCTGAAGTGC AGCGACGAGC TGGCGAACAA CGGCACCATG
421 GGCAACAACG TGACCACCGA GGAGAAGGGC ATGAAGAAGT GCAGCTTCAA CGTGACCACC
481 GTGCTGAAGG ACAAGAAGCA GCAGGTGTAC GCCCTGTTCT ACCGCTTGA CATCGTGCCC
541 ATCGACAACG ACAGCAGCAC CAACAGCACC AACTACCGCC TGATCAACTG CAACACCAGC
601 GCCATCACCC AGGCCTGCCC CAAGGTGAGC TTCGAGCCCA TCCCCTCCA CTACTGCGCC
661 CCCGCCGGCT TCGCCATCCT GAAGTGCCGC GACAAGAAGT TCAACGGCAC CGGCCCTGCG
721 ACCAACGTGA GCACCGTGCA GTGCACCCAC GGCATCCGCC CCGTGGTGAG CACCCAGCTG
781 CTGCTGAACG GCAGCCTGGC CGAGGAGGAG GTGATCATCC GCAGCGAGAA CCTGACCAC
841 AACGCCAAGA ACATCATCGC CCACCTGAAC GAGAGCGTGA AGATCACCTG CGCCCGCCCC
901 TACCAGAACA CCCGCCAGCG CACCCCATC GGCCTGGGCC AGAGCCTGTA CACCACCCGC
961 AGCCGCAGCA TCATCGGCCA GGCCCACTGC AACATCAGCC GCGCCAGTG GAGCAAGACC
1021 CTGCAGCAGG TGGCCCGCAA GCTGGGCACC CTGTGAACA AGACCATCAT CAAGTTCAAG
1081 CCCAGCAGCG GCGGCGACCC CGAGATCACC ACCCACAGCT TCAACTGCGG CGGCGAGTTC
1141 TTCTACTGCA ACACCAGCGG CCTGTTCAAC AGCACCTGGA ACATCAGCGC CTGGAACAAC
1201 ATCACCAGAG GCAACAACAG CACCAACACC AACATACCC TGCAGTGCCG CATCAAGCAG
1261 ATCATCAAGA TGGTGGCCGG CCGCAAGGCC ATCTACGCCC CCCCATCGA GCGCAACATC
1321 CTGTGCAGCA GCAACATCAC CGGCCTGCTG CTGACCCGCG ACGGCGGCAT CAACAACAGC
1381 ACCAACGAGA CCTTCCGCCC CGGCGGCGGC GACATGCGCG ACAACTGGCG CAGCGAGCTG
1441 TACAAGTACA AGGTGGTGCA GATCGAGCCC CTGGGCGTGG CCCCCACCCG CGCCAAGCGC
1501 CGCGTGGTGG AGCGCGAGAA GCGCGCCATC GGCTGGGCG CCATGTTTCT GGGCTTCTTG
1561 GCGCGCCGCG GCAGCACCAT GGGCGCCGCG AGCGTGACCC TGACCGTGCA GGCCCGCCAG
1621 CTGATGAGCG GCATCGTGCA GCAGCAGAAC AACCTGCTGC GCGCCATCGA GGCCAGCAG
1681 CACCTGCTGC AGCTGACCGT GTGGGGCATC AAGCAGCTGC AGGCCCCGAT CCTGGCCGTG
1741 GAGCGCTACC TGAAGGACCA GCAGCTGCTG GGCATCTGGG GCTGCAGCGG CAAGCACATC
1801 TGCACCACCA ACGTGCCCTG GAACAGCAGC TGGAGCAACC GCAGCCTGAA CGAGATCTGG
1861 CAGAACATGA CCTGGATGGA GTGGGAGCGC GAGATCGACA ACTACACCGG CCTGATCTAC
1921 AGCCTGATCG AGGAGAGCCA GACCCAGCAG GAGAAGAAGC AGAAGGAGCT GCTGGAGCTG
1981 GACAAGTGGG CCAGCCTGTG GAACTGGTTC AGCATCACCC AGTGGCTGTG GTACATCAAG
2041 ATCTTCATCA TGATCATCGG CGGCCTGATC GGCCTGCGCA TCGTGTTTCG CGTGCTGAGC
2101 CTGGTGAAAC GCGTGCGCCA GGGCTACAGC CCCCTGAGCT TCCAGACCCT GCTGCCCGCC
2161 CCCC GCGGCC CCGACCGCCC CGAGGGCACC GAGGAGGAGG GCGGCGAGCG CGGCCGCGAC
2221 CGCAGCGTGC GCCTGTGAA CGGCTTACG GCCCTGATCT GGGACGACCT GCGCAGCCTG
2281 TGCCCTGTTCA GCTACCACCG CCGCGCGAC CTGATCCTGA TCGCCGTGCG CATCGTGGAG
2341 CTGCTGGGCC GCCGCGGCTG GGACATCCTG AAGTACCTGT GGAACCTGCT GCAGTACTGG
2401 AGCCAGGAGC TGGCGAACAG CGCCAGCAGC CTGTTGAGC CCATCGCCAT CGCCGTGGCC
2461 GAGGGCACCG ACCGCGTGAT CGAGATCATC CAGCGCGCCT GCGCGCCGCT GCTGAACATC
2521 CCCC GCGCCA TCCGCCAGGG CCTGGAGCGC AGCCTGCTGT AA

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**FIGURE 17**

gp160mod.93IN101

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1 ATGCGCGTGC GCGGCACCCT GCGCAACTAC CAGCAGTGGT GGATCTGGGG CGTGCTGGGG
61 TTCTGGATGC TGATGATCTG CAACGGCGGC GGCAACCTGT GGGTGACCGT GTACTACGGC
121 GTGCCCCTGT GGAAGGAGGC CAAGACCACC CTGCTGTGCG CCAAGCGACGC CAAGGCCTAC
181 GAGCGCGAGG TGCACAACGT GTGGGCCACC CACGCCTGCG TGCCCACCGA CCCCACCC
241 CAGGAGATCG TGCTGGGCAA CGTGACCGAG AACTTCAACA TGTGGAAGAA CGACATGGTG
301 GACCAGATGC ACGAGGACGT GATCAGCCTG TGGGACCAGA GCCTGAAGCC CTGCGTGAAG
361 CTGACCCCCC TGTGCGTGAC CCTGGAGTGC CGCAACGTGA GCCGCAACGT GAGCAGCTAC
421 AACACCTACA ACGGCAGCGT GGAGGAGATC AAGAAGTGCA GCTTCAACGC CACCCCGAG
481 GTGCGCGACC GCAAGCAGCG CATGTACGCC CTGTTCTACG GCCTGGACAT CGTGCCCTG
541 AACAGAAGA ACAGCAGCGA GAACAGCAGC GAGTACCGCC TGATCAACTG CAACACCAGC
601 GCCATCACCC AGGCCTGCC CCAAGGTGACC TTCGACCCCA TCCCCATCCA CTA CTGCGCC
661 CCCGCCGGCT ACGCCATCCT GAAGTGCAAC AACAAGACCT TCAACGGCAC CGGCCCTGC
721 AACACGTGA GCACCGTGCA GTGCACCCAC GGCATCAAGC CCGTGGTGAG CACCCAGCTG
781 CTGCTGAACG GCAGCCTGGC CGAGGGCGAG ATCATCATCC GCAGCGAGAA CCTGACCAAC
841 AACGTGAAGA CCATCATCGC GCACCTGAAC CAGAGCGTGG AGATCGTGTG CACCGGCC
901 AACACAACA CCCCAAGAG CATCCGCATC GGCCCCGGCC AGACCTTCTA CGCCACCGGC
961 GACATCATCG GCGACATCCG CCAGGCCAC TGCAACATCA GCCGCGACAA GTGGAACGAG
1021 ACCCTGCAGC GCGTGGGCAA GAAGCTGGCC GAGCACTTCC ACAACAAGC CATCAAGTTC
1081 GCCAGCAGCA CGGCGGCGCA CCTGGAGATC ACCACCCACA GCTTCAACTG CCGCGCGAG
1141 TTCTTCTACT GCAACACCAG CGGCCTGTTC AACGGCACCT ACATGCCCAC CTACATGCCC
1201 AACGGCACCG AGAGCAACAG CAACAGCACC ATCACCATCC CCTGCCGCAT CAAGCAGATC
1261 ATCAACATGT GGCAGGAGGT GGGCCGCGCC ATGTACGCCC CCCCATCGC CGGCAACATC
1321 ACCTGCACCA CCAACATCAC CGCCCTGCTG CTGGTGACG ACGGCGGCAT CAAGGAGAAC
1381 GACACCGAGA ACAAGACCGA GATCTTCCGC CCCGGCGGCG GCGACATGCG CGACAACCTGG
1441 CGCAGCGAGC TGTACAAGTA CAAGGTGGTG GAGATCAAGC CCTGGGCGT GGCCCCACC
1501 GCCGCCAAGC GCCGCGTGGT GGAGCGCGAG AAGCGCGCCG TGGGCATCGG CGCCGTGTT
1561 CTGGGCTTCC TGGGCGCCGC CGGCAGCACC ATGGGCGCCG CCAGCATCAC CCTGACCGCC
1621 CAGGCCCGCC AGCTGCTGAG CGGCATCGTG CAGCAGCAGA GCAACCTGCT GCGCGCCATC
1681 GAGGCCAGC AGCACCTGCT GCAGCTGACC GTGTGGGGCA TCAAGCAGCT GCAGACCGC
1741 GTGCTGGCCA TCGAGCGCTA CCTGAAGGAC CAGCAGCTGC TGGGCATCTG GGGCTGCAGC
1801 GGCAAGCTGA TCTGCACCAC CGCCGTGCCC TGGAAACAGCA GCTGGAGCAA CAAGACCCAG
1861 AGCGAGATCT GGAACAACAT GACCTGGATG CAGTGGGACC GCGAGGTGAG CAACTACACC
1921 AACATCATCT ACAGCCTGCT GGAGGAGAGC CAGAACCAGC AGGAGAAGAA CGAGAAGGAC
1981 CTGCTGGCCC TGGACAGCTG GAAGAACCCT TGGAGCTGGT TCGACATCAC CAACTGGCTG
2041 TGGTACATCA AGATCTTCAT CATGATCGTG GCGGCGCTGA TCGGCCTGCG CATCATCTTC
2101 GCCGTGTGA GCATCGTGAA CCGCGTGCGC CAGGGCTACA GCCCCCTGAG CTTCCAGACC
2161 CTGACCCCA ACCCCGCGG CCCCAGCCGC CTGGGCGGCA TCGAGGAGGA GGGCGGCGAG
2221 CAGGACAAGG ACCGCAGCAT CGCCTGGTG AACGGCTTCC TGGCCCTGGC CTGGGACGAC
2281 CTGCGCAACC TGTGCTGTT CAGTACCAC CGCCTGCGC ACTTCATCA CGTGGCCGCC
2341 CGCGTGGTGG AGCTGCTGGG CCGCAGCAGC TGGGAGGCCC TGAAGTACCT GGGCAGCCTG
2401 GTGCAGTACT GGGGCTGGA GCTGAAGAAG AGCGCCATCA GCCTGTTCGA CAGCATCGCC
2461 ATCGTGGTGG CCGAGGGCAC CGACCGCATC ATCGAGCTGG TGCAGGGCTT CTGCCGCGCC
2521 ATCCGCAACA TCCCACCCG CATCCGCCAG GGCTTCGAGG CCGCCCTGCA GTAA

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**FIGURE 18**  
gp160mod.cm235.V3con

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1 ATGGATGCAA TGAAGAGAGG GCTCTGCTGT GTGCTGCTGC TGTGTGGAGC AGTCTTCGTT
61 TCGCCAGCG CTAGCAACAA CCTGTGGGTG ACCGTGTACT ACGGCGTGCC CGTGTGGCGC
121 GACGCCGACA CCACCTGTGT CTGCGCCAGC GACGCCAAGG CCCACGAGAC CGAGGTGCAC
181 AACGTGTGGG CCACCCACGC CTGCGTGCCC ACCGACCCCA ACCCCAGGA GATCCACCTG
241 GAGAACGTGA CCGAGAACTT CAACATGTGG AAGAACAACA TGGTGGAGCA GATGCAGGAG
301 GACGTGATCA GCCTGTGGGA CCAGAGCCTG AAGCCCTGCG TGAAGCTGAC CCCCCTGTGC
361 GTGACCCTGA ACTGCACCAA CGCCAGCTG ACCAACGTGA ACAACATCAC CAGCGTGAGC
421 AACACCATCG GCAACATCAC CGACGAGGTG CGCAACTGCA GCTTCAACAT GACCACCGAG
481 CTGCGCGACA AGAAGCAGAA GGTGCACGCC CTGTTCTACA AGCTGGACAT CGTGCCCATC
541 GAGGACAACA AGACCAGCAG CGAGTACCGC CTGATCAACT GCAACACCAG CGTGATCAAG
601 CAGGCCTGCC CCAAGATCAG CTTCGACCCC ATCCCCATCC ACTACTGCAC CCCCGCCGGC
661 TACGCCATCC TGAAGTGCAA CGACAAGAAC TTCAACGGCA CCGGCCCTG CAAGAACGTG
721 AGCAGCGTGC AGTGCACCCA CGGCATCAAG CCCGTGGTGA GCACCGAGCT CGTGCTGAAC
781 GGCAGCCTGG CCGAGGAGGA GATCATCATC CGCAGCGAGA ACCTGACCAA CAACGCCAAG
841 ACCATCATCG TGCACCTGAA CAAGAGCGTG GAGATCAACT GCACCCGCCC CAGCAACAAC
901 ACCGCACCA GCATACCAT CGGCCCGGC CAGGTGTTCT ACCGCACCGG CGACATCATC
961 GGCACATCC GCAAGGCTA CTGCGAGATC AACGGCACA AGTGGAACTG GCAGGGCGCC
1021 CAGGTGACCG AGAAGCTGAA GGAGCACTTC AACACAAGA CCATCATCTT CCAGCCCCC
1081 AGCGCGGCG ACCTGGAGAT CACCATGCAC CACTTCAACT GCCCGGCGA GTTCTTCTAC
1141 TGCAACACCA CCGCCTGT CAACAACACC TGCATCGAGA ACGGCACCAT GGGCGGCTGC
1201 AACGGCACA TCATCCTGCC CTGCAAGATC AAGCAGATCA TCAACATGTG GCAGGGCGCC
1261 GGCAGGCCA TGTACGCCCC CCCATCAGC GGCCGCATCA ACTGCGTGAG CAACATCACC
1321 GGCATCCTGC TGACCCGCGA CGGCGCGGCC ATCAACACCA CCAACGAGAC CTTCCGCCCC
1381 GGCAGCGCA ACATCAAGGA CAACTGGCGC AGCGAGCTGT ACAAGTACAA GGTGGTGCAG
1441 ATCGAGCCCC TGGGCATCGC CCCCACCGC GCCAAGCGCC GCGTGGTGA GCGCGAGAAG
1501 CGCGCCGTGG GCATCGGCGC CATGATCTTC GGCTTCCTGG GCGCCGCGG CAGCACCATG
1561 GGCAGCGCA GCATACCCCT GACCGTGAG GCGCGCCAGC TGCTGAGCGG CATCGTGAG
1621 CAGCAGAGCA ACCTGCTGCG CGCCATCGAG GCCCAGCAGC ACCTGCTGCA GCTGACCGTG
1681 TGGGGCATCA AGCAGCTGCA GGCCCGCGTG CTGGCCGTGG AGCGCTACCT GAAGGACCAG
1741 AAGTTCCTGG GCCTGTGGGG CTGACGCGG AAGATCATCT GCACCACCGC CGTGCCCTGG
1801 AACAGCACCT GGAGCAACCG CAGCTACGAG GAGATCTGGA ACAACATGAC CTGGATCGAG
1861 TGGGAGCGCG AGATCAGCAA CTACACCAAC CAGATCTACG AGATCCTGAC CGAGAGCCAG
1921 AACAGCAGG ACCGCAACGA GAAGGACCTG CTGGAGCTGG ACAAGTGGG CAGCCTGTGG
1981 AACTGGTTTC ACATCACCAG GTGGCTGTGG TACATCAAGA TCTTCATCAT GATCATCGGC
2041 GGCCTGATCG GCCTGCGCAT CATCTTCGCC GTGCTGAGCA TCGTGAACCG CGTGCGCCAG
2101 GGCTACAGCC CCTGAGCTT CCAGACCCCC TTCCACCACC AGCGCGAGC CGACCCGAGC
2161 GAGCGCATCG AGGAGGGCGG CGGCGAGCAG GGCCGCGACC GCAGCGTGCG CCTGGTGAGC
2221 GGCTTCCTGG CCTGGGCTG GGACGACCTG CGCAGCCTGT GCCTGTTCAG CTACCACCGC
2281 CTGCGCGACT TCATCCTGAT CGCCGCGCGC ACGGTGAAGC TGCTGGGCGG CAGCAGCCTG
2341 AAGGGCCTGC GCCGCGGCTG GGAGGGCCTG AAGTACCTGG GCAACCTGCT GCTGTACTGG
2401 GGCCAGGAGC TGAAGATCAG CGCCATCAGC CTGCTGGACG CCACCGCAT CATCGTGCC
2461 GGCTGGACCG ACCGCGTGAT CGAGGTGGCC CAGGGCGCCT GGCAGCCAT CCTGCACATC
2521 CCGCGCGCA TCCGCCAGGG CCTGGAGCGC ACCCTGCTGT AA

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**FIGURE 19**

gp160partialmod.cm235.V3 con

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1  ATGGATGCAA TGAAGAGAGG GCTCTGCTGT GTGCTGCTGC TGTGTGGAGC AGTCTTCGTT
61  TCGCCAGCG CTAGCAACAA CTTGTGGGTT ACAGTTTATT ATGGGGTTCC TGTGTGGAGA
121 GATGCAGATA CCACCCATT TGTGTCATCA GATGCCAAAG CACATGAGAC AGAAGTGCAC
181 AATGTCTGGG CCACACATGC CTGTGTACCC ACAGACCCCA ACCACAAGA AATACACCTG
241 GAAAATGTAA CAGAAAATTT TAACATGTGG AAAAATAACA TGGTAGAGCA GATGCAGGAG
301 GATGTAATCA GTTTATGGGA TCAAAGTCTA AAGCCATGTG TAAAGTTAAC TCCTCTCTGC
361 GTTACTTTAA ATTGTACCAA TGCTAAGTTG ACCAATGTCA ATAACATAAC CAGTGTCTCT
421 AACACAATAG GAAATATAAC AGATGAAGTA AGAACTGTT CTTTTAATAT GACCACAGAA
481 CTAAGAGATA AGAAGCAGAA GGTCCATGCA CTTTTTTATA AGCTTGATAT AGTACCAATT
541 GAAGATAATA AGACTAGTAG TGAGTATAGG TTAATAAATT GTAATACTTC AGTCATTAAG
601 CAGGCTTGTC CAAAGATATC CTTTGATCCA ATTCCTATAC ATTATGTAC TCCAGCTGGT
661 TATGCGATTT TAAAGTGTAA TGATAAGAA TTTCAATGGGA CAGGGCCATG TAAAAATGTC
721 AGCTCAGTAC AATGCACACA TGGAAATTAAG CCAAGTGGTAT CAACTCAATT GCTGTTAAAT
781 GGCAGTCTAG CAGAAGAAGA GATAATAATC AGATCTGAAA ATCTCACAAA CAATGCCAAA
841 ACCATAATAG TGCACCTTAA TAAATCTGTA GAAATCAATT GTACCAGACC CTCCAACAAT
901 ACAAGAACAA GTATAACTAT AGGACCAGGA CAAGTATTCT ATAGAACAGG AGACATAATA
961 GGAGATATAA GAAAAGCATA TTGTGAGATT AATGGAACAA AATGGAATGA AGTTTAAACA
1021 CAGGTAAC TG AAAAATTAAA AGAGCACTTT AATAATAAGA CAATAATCTT TCAACCACCC
1081 TCAGGAGGAG ATCTAGAAAT TACAATGCAT CATTTTAATT GTAGAGGGGA ATTTTCTAT
1141 TGCAATACAA CACGACTGTT TAATAATACT TGCATAGAAA ATGGAACCAT GGGGGGGTGT
1201 AATGGCACTA TCATACTTCC ATGCAAGATA AAGCAAATTA TAAACATGTG GCAGGGAGCA
1261 GGACAAGCAA TGTATGCTCC TCCCATCAGT GGAAGAATTA ATTGTGTATC AAATATTACA
1321 GGAATACTAT TGACAAGAGA TGGTGGTGCT ATTAATACAA CTAATGAGAC CTTCCGCCCC
1381 GCGGCGCGCA ACATCAAGGA CAACTGGCGC AGCGAGCTGT ACAAGTACAA GGTGGTGCAG
1441 ATCGAGCCCC TGGGCATCGC CCCCACCCGC GCCAAGCGCC GCGTGGTGGG GCAGGAGAAG
1501 CGCGCCGTGG GCATCGGCGC CATGATCTTC GGCTTCCTGG GCGCCGCCGG CAGCACCATG
1561 GCGCGCCGCA GCATCACCC TACCCTGCAG GCCCGCCAGC TGCTGAGCGG CATCGTGCG
1621 CAGCAGAGCA ACCTGCTGCG CGCCATCGAG GCCCAGCAGC ACCTGCTGCA GCTGACCGTG
1681 TGGGGCATCA AGCAGCTGCA GGCCCGCGTG CTGGCCGTGG AGCGCTACCT GAAGGACCAG
1741 AAGTTCCTGG GCCTGTGGGG CTGCAGCGGC AAGATCATCT GCACCACCGC CGTGCCCTGG
1801 AACAGCACCT GGAGCAACCG CAGCTACGAG GAGATCTGGA ACAACATGAC CTGGATCGAG
1861 TGGGAGCGCG AGATCAGCAA CTACACCAAC CAGATCTACG AGATCTTGAC CGAGAGCCAG
1921 AACCAGCAGG ACCGCAACGA GAAGGACCTG CTGGAGCTGG ACAAGTGGGC CAGCCTGTGG
1981 AACTGGTTCG ACATCACCAA GTGGCTGTGG TACATCAAAA TATTATAAT GATAATAGGA
2041 GGTTTAATAG GTTTAAGGAT AATTTTGTCT GTGCTTTCTA TAGTGAATAG AGTTAGGCAG
2101 GGATACTCAC CTTTGTCTTT CCAGACCCCT TTCCATCATC AGAGGGAACC CGACAGATCC
2161 GAAAGAATCG AAGAAGGAGG TGGCGAGCAA GGCAGAGACA GATCCGTGCG ATTAGTGAGC
2221 GGATTCTTAG CTCTTGCGTG GGACGATCTA CGGAGCCTGT GCCTCTTACG CTACCACCGC
2281 TTGAGAGACT TCATCTTGAT TGCAGCGAGG ACTGTGAAAC TTCTGGGACG CAGCAGTCTC
2341 AAGGGACTGA GACGGGGGTG GGAAGGTCTC AAATATCTGG GGAATCTTCT GTTATATTGG
2401 GGTCAGGAAC TAAAAATTAG CGCTATTCTT TTGCTTGATG CTACAGCAAT AATAGTAGCG
2461 GGGTGGACAG ATAGGGTTAT AGAAGTAGCA CAAGGAGCTT GGAGAGCCAT TCTCCACATA
2521 CCTAGGAGAA TCAGACAGGG CTTAGAAAGG ACTTGCTAT AA

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FIGURE 20

Serum Binding Antibody Titers to HIV-1<sub>SF162</sub> ENV Protein

Immunization	Replication-Competent Ad		Replication-Defective Ad	
	10 <sup>7</sup>	10 <sup>8</sup>	10 <sup>7</sup>	10 <sup>8</sup>
Post 1 <sup>st</sup> Ad	20	114.11	276.00	46.11
	20	390.91	N/A	72.06
	20	33.31		29.51
Post 2 <sup>nd</sup> Ad	2315.60	4242.53	114	55.57
	14380.44	8251.33	N/A	128.00
	372.87	2181.35		24.13
Post 1 <sup>st</sup> gp140	41175.45	43589.41	906	2675.15
	42411.99	51950.41	N/A	9448.33
	39974.95	36574.05		757.43
Post 2 <sup>nd</sup> gp140	19789.57	65799.55	14176	105578.03
	32906.06	68333.17	N/A	208905.20
	11901.37	63359.86		53357.79

FIGURE 21

Proliferative responses following Ad-HIVenv recombinant priming and HIV<sub>SF162</sub> oligomeric gp140 $\Delta$ V2 boosting

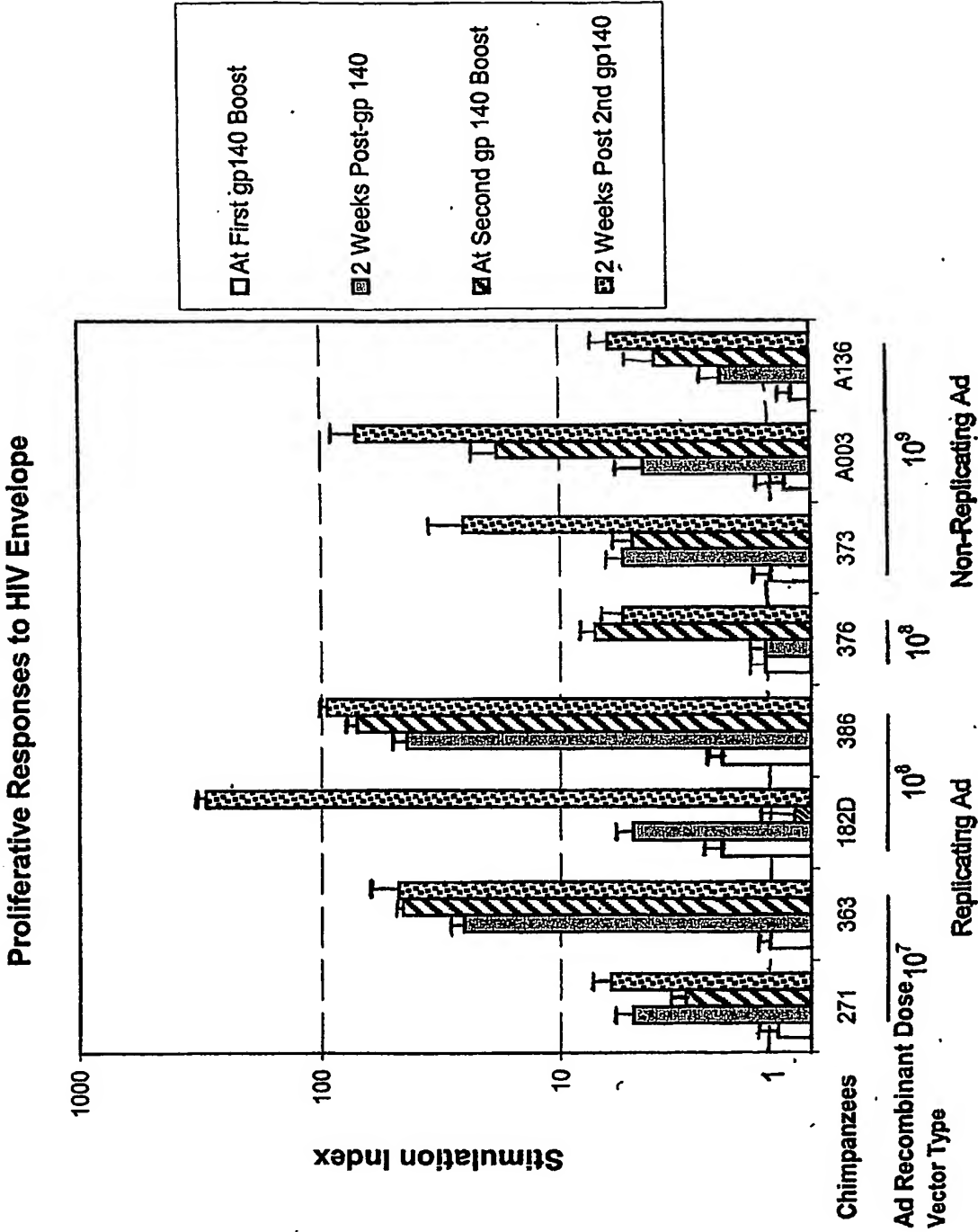
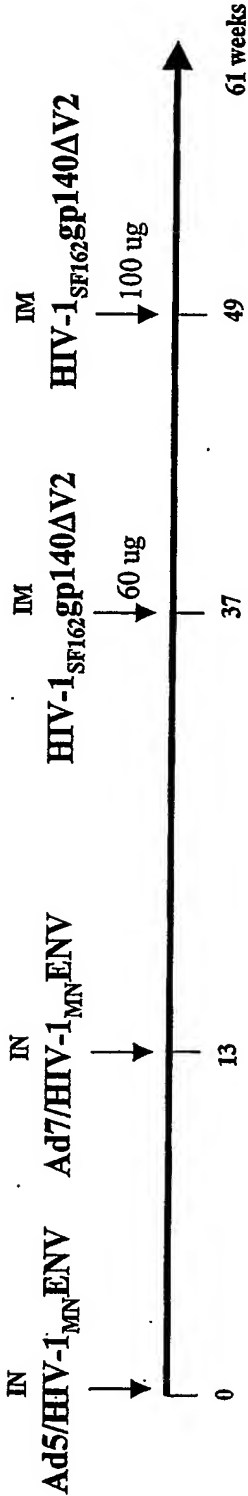


FIGURE 22

Immunization Regimen and Schedule



IN = intranasal; IM = intramuscular

Replication-competent Ad Vaccine Group		Replication-defective Ad Vaccine Group	
Chimpanzees	Priming Immunization (dose)	Chimpanzees	Priming Immunization (dose)
271, 363, A163	Ad5- or Ad7-ΔE3/HIV <sub>MN</sub> Env (10 <sup>7</sup> pfu)	376, 360	Ad5- or Ad7-ΔE1E3/HIV <sub>MN</sub> Env (10 <sup>8</sup> pfu)
182D, 386	Ad5- or Ad7-ΔE3/HIV <sub>MN</sub> Env (10 <sup>8</sup> pfu)	373, A136, A003	Ad5- or Ad7-ΔE1E3/HIV <sub>MN</sub> Env (10 <sup>9</sup> pfu)

Priming with replicating Ad-recombinant results in higher binding antibody titers

FIGURE 23A

Serum Binding Antibody Titers to HIV-1<sub>SF162</sub> Env Protein

Animal Groups	Dose	2 <sup>nd</sup> Ad wk 15	1 <sup>st</sup> gp140 wk 39	2 <sup>nd</sup> gp140 wk 51
Replicating Ad	10 <sup>7</sup>	475	3237	13462
Replicating Ad	10 <sup>8</sup>	4242	43589	65799
Non-replicating Ad	10 <sup>8</sup>	48	2784	21953
Non-replicating Ad	10 <sup>9</sup>	56	2672	49005

\*\* Higher titers to gp120 homologous to gp140 boost independent of vector (P = 0.0040)

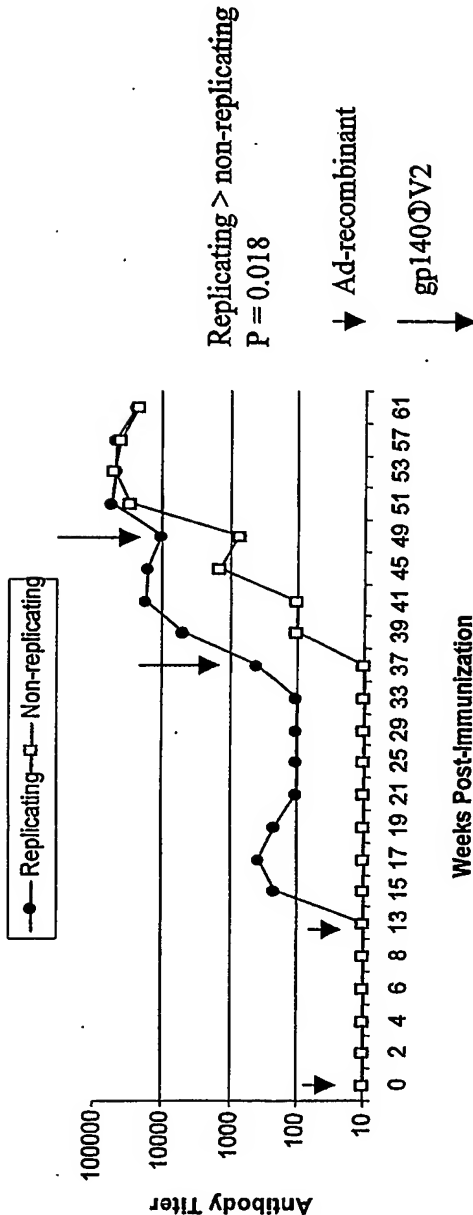
Serum Binding Antibody Titers to HIV-1<sub>MB</sub> Env Protein

Animal Groups	Dose	2 <sup>nd</sup> Ad wk 15	1 <sup>st</sup> gp140 wk 39	2 <sup>nd</sup> gp140 wk 51
Replicating Ad	10 <sup>7</sup>	397	3794	28360
Replicating Ad	10 <sup>8</sup>	68	4021	213307
Non-replicating Ad	10 <sup>8</sup>	10	51	10471
Non-replicating Ad	10 <sup>9</sup>	22	161	49570

29/35  
\* Higher titers to gp120 heterologous to gp140 boost in groups primed with replicating Ad-recombinants (P = 0.018).

FIGURE 23B

Kinetics of Serum Binding Antibody Titers to HIV-1<sub>MB</sub> Env Protein





Induction of Cross-Clade Binding Antibodies

FIGURE 24A

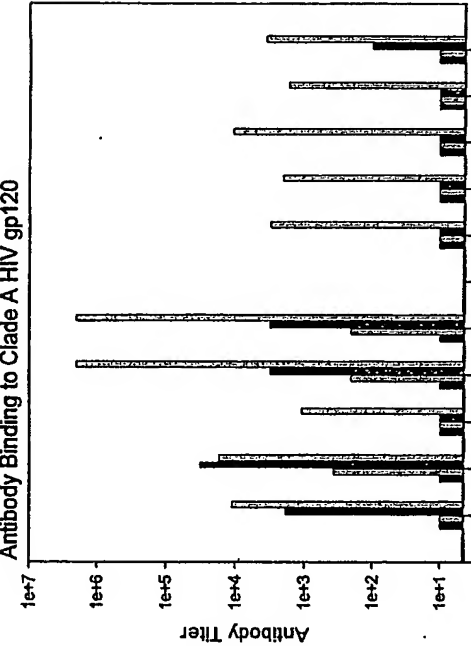


FIGURE 24C

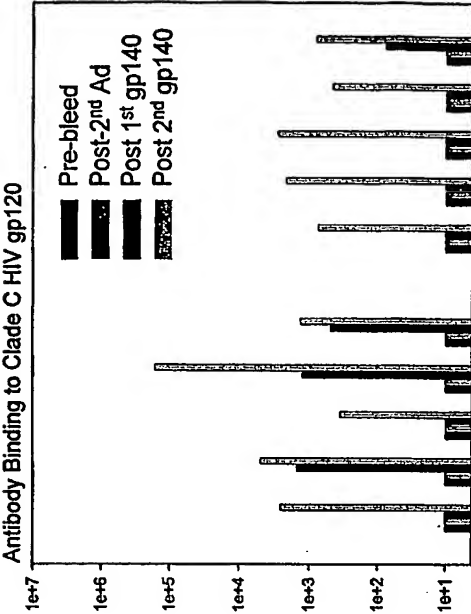
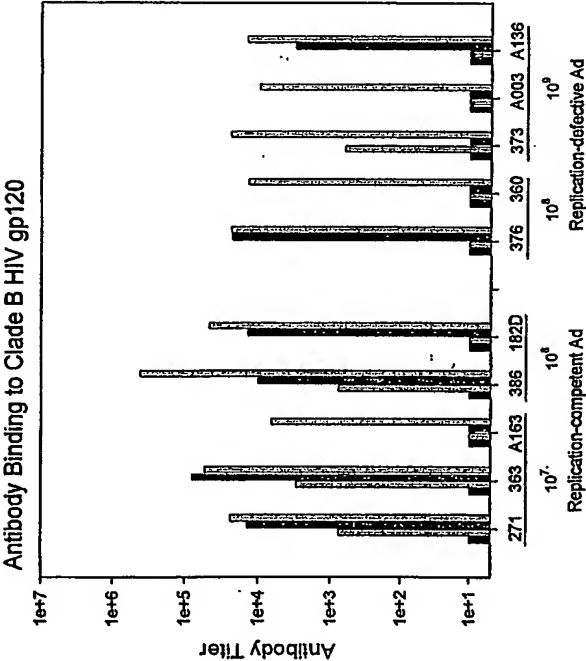
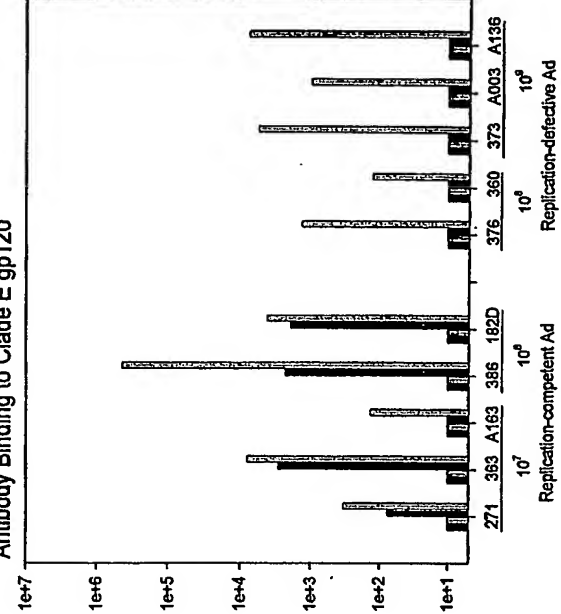


FIGURE 24B



Antibody Binding to Clade E gp120



**Replicating Ad-HIV recombinants are more effective  
at priming neutralizing antibody responses**

FIGURE 25A

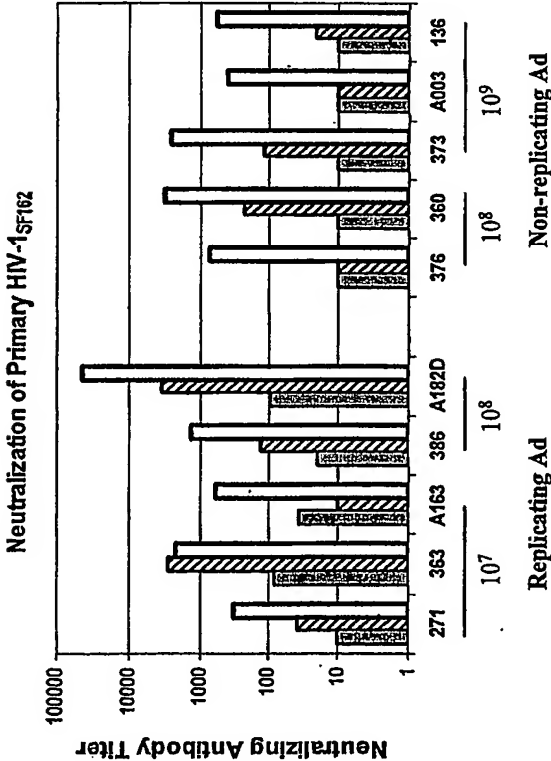
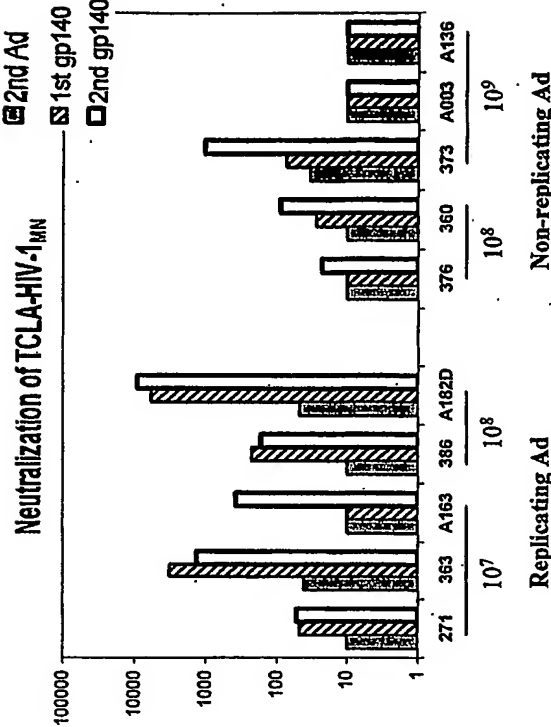


FIGURE 25B



Replicating > non-replicating; p = 0.012

FIGURE 26

Induction of neutralizing antibodies to clade C HIV<sub>TV-1</sub> following a clade B immunization regimen.

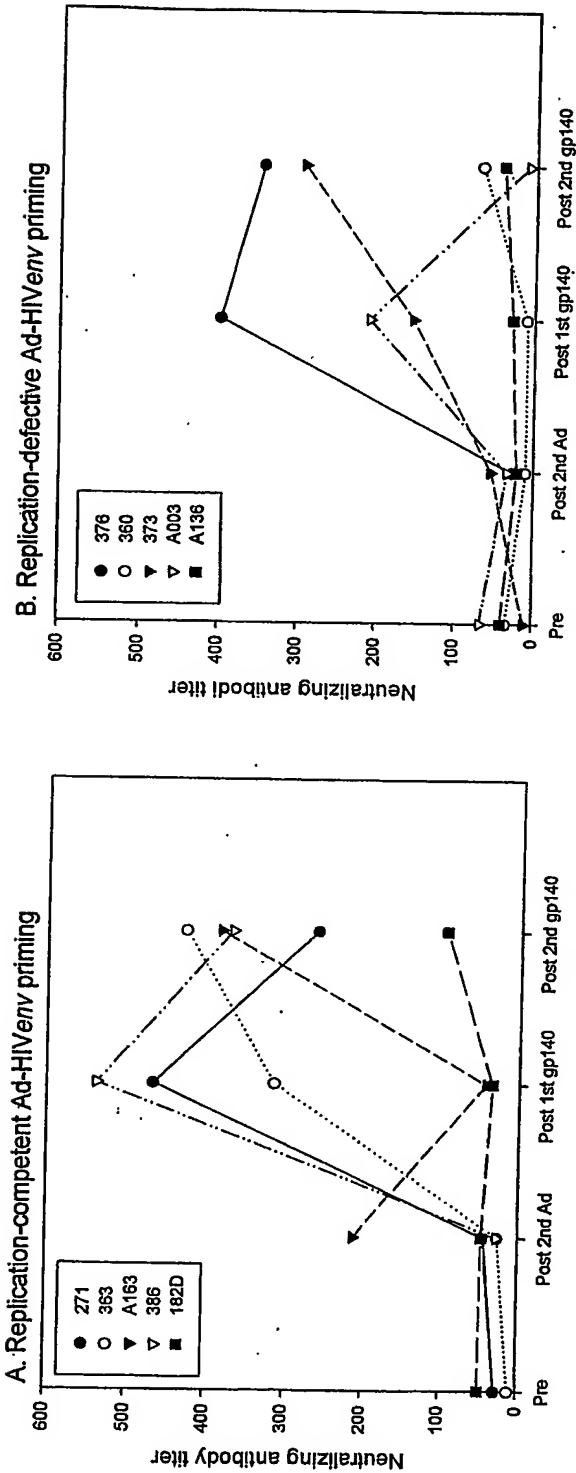
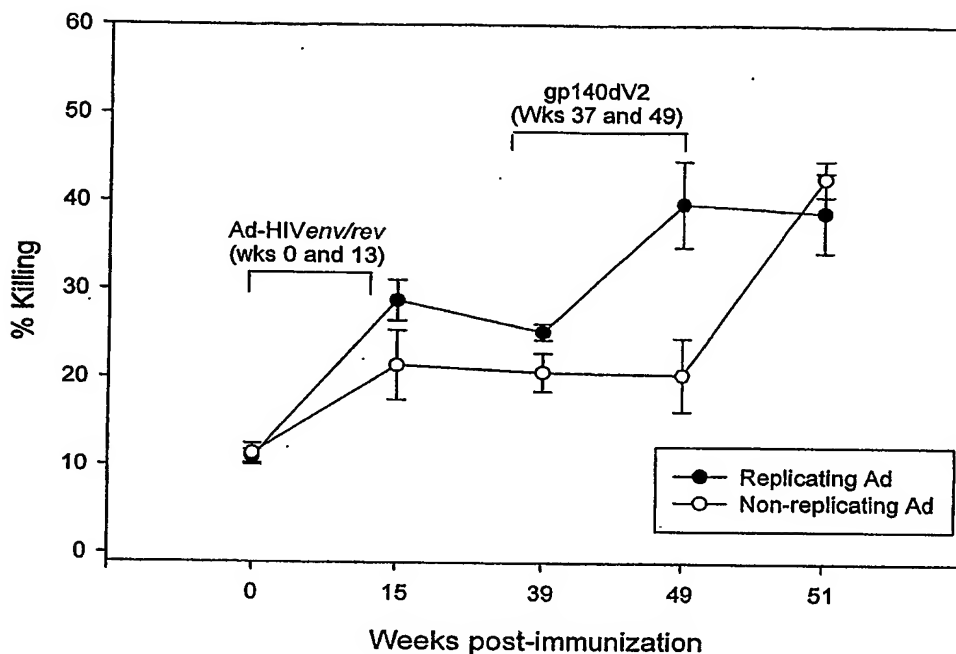


FIGURE 27

Induction of antibody-dependent cellular cytotoxicity (ADCC) activity by an Ad-HIV<sub>MN</sub>*env/rev* priming/oligomeric gp140dV2 boosting regimen

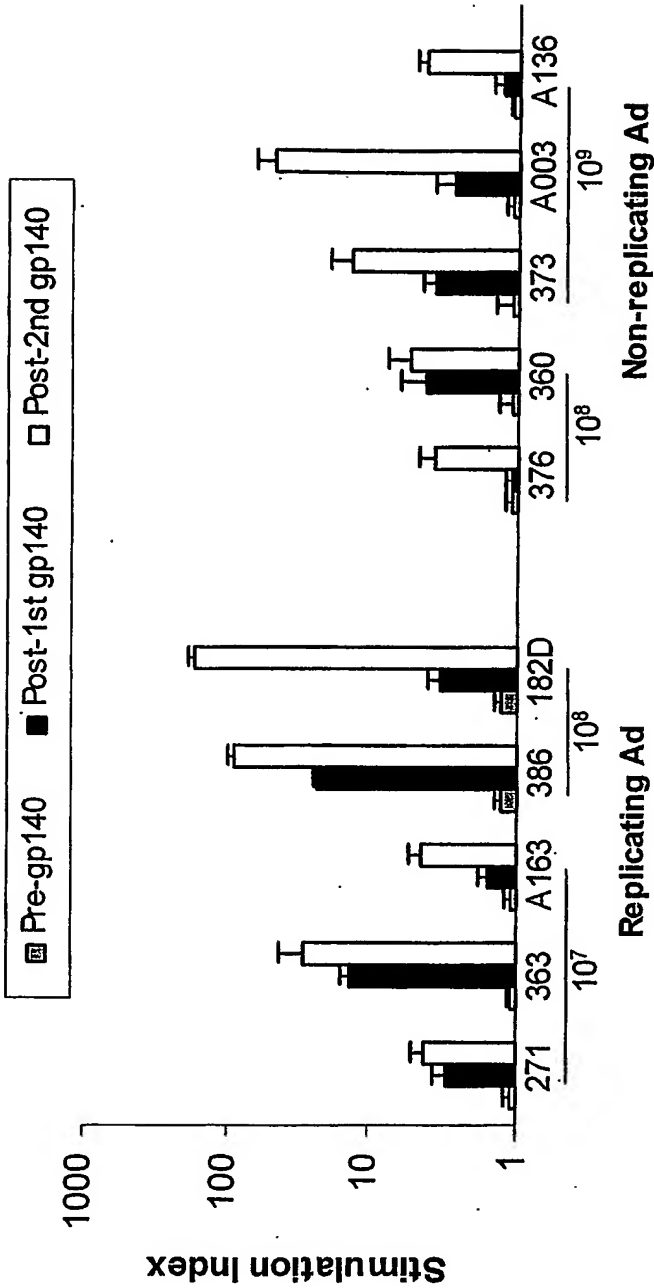


Chimpanzees were immunized intranasally with Ad5-HIV<sub>MN</sub>*env/rev* (wk 0) and with Ad7-HIV<sub>MN</sub>*env/rev* (wk 13). They were boosted with oligomeric HIV<sub>SF162</sub> gp140 dV2 in MF-59 adjuvant at weeks 37 and 49. ADCC activity was determined using human PBMC as effectors and HIV<sub>IIIB</sub> gp120-coated CEM-NK<sup>+</sup> cells at an E:T of 50:1. Ten-fold serum dilutions were evaluated. Positive killing was defined as % killing by the negative control + 3 S.D. (20.4%).

A significant increase in % killing over weeks 15 to 51 was seen in chimpanzees primed with the replication-competent Ad-recombinants compared to the replication-defective Ad-recombinants ( $P = 0.022$ ).

FIGURE 28

Replicating Ad-HIV recombinants are better at priming T-cell proliferative responses than non-replicating Ad-HIV recombinants



Post-2<sup>nd</sup> gp140: Replicating > Non-replicating,  $p = 0.022$   
Over all 3 time points, there is a linear trend of replicating > non-replicating,  $p = 0.010$

FIGURE 29  
Replicating Ad /HIV<sub>MN</sub>*env/rev* Induces More IFN- $\gamma$  Secreting Cells at the Same or Lower Dose Compared to Non-replicating Ad /HIV<sub>MN</sub>*env/rev*

